

(21)(A1) 2,269,105

(22) 1999/04/29

(43) 2000/04/14

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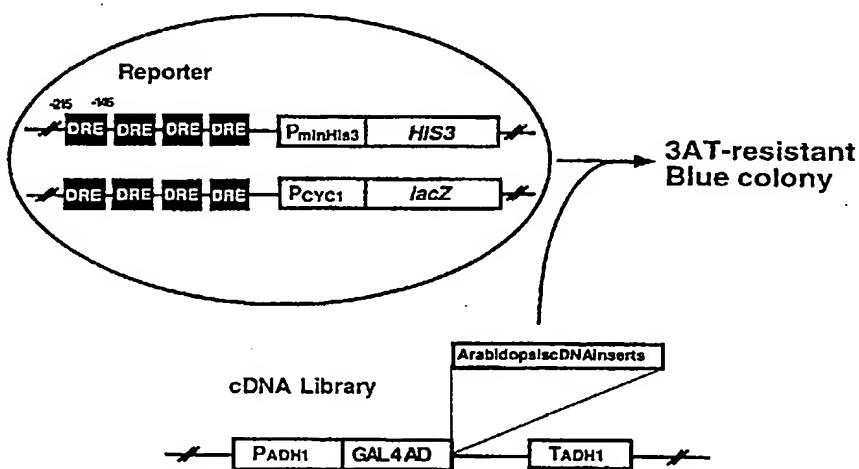
(51) Int.Cl.⁶ A01H 5/00

(30) 1998/10/14 (292348/1998) JP

(54) PLANTES TOLERANTES AU STRESS ENVIRONNEMENTAL

(54) ENVIRONMENTAL STRESS-TOLERANT PLANTS

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(57) The present invention relates to an environmental stress-tolerant plant. The invention discloses a transgenic plant containing a gene in which a DNA encoding the following protein (a) or (b) is ligated downstream of a stress responsive promoter: (a) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10; (b) a protein which consists of the amino acid sequence having deletion, substitution or addition of at least one amino acid in the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10 and which regulates the transcription of genes located downstream of a stress responsive element.

ABSTRACT

The present invention relates to an environmental stress-tolerant plant. The invention discloses a transgenic plant containing a gene in which a DNA encoding the following protein (a) or (b) is ligated downstream of a stress responsive promoter:

- (a) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10;
- (b) a protein which consists of the amino acid sequence having deletion, substitution or addition of at least one amino acid in the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10 and which regulates the transcription of genes located downstream of a stress responsive element.

ENVIRONMENTAL STRESS-TOLERANT PLANTS

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to a transgenic plant containing a gene in which a DNA encoding a protein that binds to dehydration responsive element (DRE) and regulates the transcription of genes located downstream of DRE is ligated downstream of a stress responsive promoter.

2. Prior Art

In the natural world, plants are living under various environmental stresses such as dehydration, high temperature, low temperature or salt. Unlike animals, plants cannot protect themselves from stresses by moving. Thus, plants have acquired various stress tolerance mechanisms during the courses of their evolution. For example, low temperature tolerant plants (Arabidopsis thaliana, spinach, lettuce, garden pea, barley, beet, etc.) have less unsaturated fatty acid content in their biomembrane lipid than low temperature sensitive plants (maize, rice, pumpkin, cucumber, banana, tomato, etc.). Therefore, even when the former plants are exposed to low temperatures, phase transition is hard to occur in their biomembrane lipid and, thus, low temperature injury does not occur easily.

To date, dehydration, low temperature or salt tolerant lines have been selected and crossed in attempts to artificially create environmental stress tolerant plants. However, a long time is needed for such selection, and the crossing method is only applicable between limited species. Thus, it has been difficult to create a

plant with high environmental stress tolerance.

As biotechnology progressed recently, trials have been made to create dehydration, low temperature or salt tolerant plants by using transgenic technology which introduces into plants a specific, heterologous gene. Those genes which have been used for the creation of environmental stress tolerant plants include synthesis enzyme genes for osmoprotecting substances (mannitol, proline, glycine betaine, etc.) and modification enzyme genes for cell membrane lipid. Specifically, as the mannitol synthesis enzyme gene, *Escherichia coli*-derived mannitol 1-phosphate dehydrogenase gene [Science 259:508-510 (1993)] was used. As the proline synthesis enzyme gene, bean-derived Δ^1 -proline-5-carboxylate synthetase gene [Plant Physiol. 108:1387-1394 (1995)] was used. As the glycine betaine synthesis enzyme gene, bacterium-derived choline dehydrogenase gene [Plant J. 12:1334-1342 (1997)] was used. As the cell membrane lipid modification enzyme gene, *Arabidopsis thaliana*-derived ω -3 fatty acid desaturase gene [Plant Physiol. 105:601-605 (1994)] and blue-green alga-derived $\Delta 9$ desaturase gene [Nature Biotech. 14:1003-1006 (1996) were used. However, the resultant plants into which these genes were introduced were unstable in stress tolerance or low in tolerance level; none of them have been put into practical use to date.

Further, it is reported that a plurality of genes are involved in the acquisition of dehydration, low temperature or salt tolerance in plants [Plant Physiol., 115:327-334 (1997)]. Therefore, a gene encoding a transcription factor capable of activating simultaneously the expression of a plurality of genes involved in the acquisition of stress tolerance has been introduced into plants, yielding plants

with high stress tolerance. However, when a gene which induces the expression of a plurality of genes is introduced into a host plant, the genes are activated at the same time. As a result, the energy of the host plant is directed to production of the products of these genes and intracellular metabolism of such gene products, which often brings about delay in the growth of the host plant or dwarfing of the plant.

OBJECTS AND SUMMARY OF THE INVENTION

It is an object of the present invention to provide a transgenic plant containing a gene in which a DNA encoding a protein that binds to a stress responsive element and regulates the transcription of genes located downstream of the element is ligated downstream of a stress responsive promoter, the transgenic plant having improved tolerance to environmental stresses (such as dehydration, low temperature and salt) and being free from dwarfing.

Toward the solution of the above problem, the present inventors have cloned a novel transcription factor gene that regulates the expression of genes involved in the acquisition of dehydration, low temperature or salt stress tolerance, and introduced into a plant this novel gene ligated downstream of a stress responsive promoter. As a result, the inventors have succeeded in creating a plant which has remarkably improved tolerance to dehydration, low temperature or salt and which is free from dwarfing. Thus, the present invention has been achieved.

The present invention relates to a transgenic plant containing a gene in which a DNA encoding the following protein (a) or (b) is ligated downstream of a stress responsive promoter:

- (a) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10;
- (b) a protein which consists of the amino acid sequence having deletion, substitution or addition of at least one amino acid in the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10 and which regulates the transcription of genes located downstream of a stress responsive element.

Further, the present invention relates to a transgenic plant containing a gene in which the following DNA (c) or (d) is ligated downstream of a stress responsive promoter:

- (c) a DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9;
- (d) a DNA which hybridizes with the DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9 under stringent conditions and which codes for a protein that regulates the transcription of genes located downstream of a stress responsive element.

Specific examples of the stress include dehydration stress, low temperature stress and salt stress.

As the stress responsive promoter, at least one selected from the group consisting of rd29A gene promoter, rd29B gene promoter, rd17 gene promoter, rd22 gene promoter, DREB1A gene promoter, cor6.6 gene promoter, cor15a gene promoter, erdl gene promoter and kin1 gene promoter may be given.

This specification includes part or all of the contents as described in the specification and/or drawings of Japanese Patent Application No. 10-292348, which is a priority document of the present application.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a diagram showing the principle of screening of DREB genes.

Fig. 2 shows the structures of probes used in a gel shift assay on the DRE-binding property of DREB1A and DREB2A proteins and presents electrophoresis photographs showing the results of the gel shift assay.

Fig. 3 presents diagrams showing the transcription activating ability of DREB1A and DREB2A proteins.

Fig. 4 is a diagram showing the structure of a CaMV35S promoter-containing recombinant plasmid to be introduced into a plant.

Fig. 5 presents electrophoresis photographs showing transcription levels of individual genes in DREB1A gene-introduced plants when stress is loaded.

Fig. 6 presents photographs showing the growth of DREB1A gene-introduced plants when freezing stress or dehydration stress is given (morphology of organisms).

Fig. 7 is a diagram showing the structure of a rd29A gene promoter-containing recombinant plasmid to be introduced into a plant.

Fig. 8 presents photographs showing the growth of pBI35S:DREB1A-introduced transgenic plants (morphology of organisms).

Fig. 9 presents photographs showing the growth of pBI29AP:DREB1A-introduced transgenic plants (morphology of organisms).

Fig. 10 presents photographs showing the survival of transgenic plants after stress loading (morphology of organisms).

DETAILED DESCRIPTION OF THE INVENTION

Hereinbelow, the present invention will be described in detail.

The transgenic plant of the invention is a environmental stress tolerant, transgenic plant created by introducing a gene in which a DNA (called "DREB gene") encoding a transcription factor that binds to a dehydration responsive element (DRE) and activates the transcription of genes located downstream of DRE is ligated downstream of a stress responsive promoter.

The DREB genes used in the invention can be cloned as described below. Of these DREB genes, DRE-binding protein 1A gene is called DREB1A gene; DRE-binding protein 1B gene is called DREB1B gene; DRE-binding protein 1C gene is called DREB1C gene; DRE-binding protein 2A gene is called DREB2A gene; and DRE-binding protein 2B gene is called DREB2B gene.

1. Cloning of DREB Gene

1-1. Preparation of mRNA and a cDNA Library from Arabidopsis thaliana

As a source of mRNA, a part of the plant of Arabidopsis thaliana such as leaves, stems, roots or flowers, or the plant as a whole may be used. Alternatively, the plant obtained by sowing seeds of Arabidopsis thaliana on a solid medium such as GM medium, MS medium or #3 medium and growing the resultant seedlings aseptically may be used. The mRNA level of DREB1A gene in Arabidopsis thaliana plants increases when they are exposed to low temperature stress (e.g. 10 to -4°C). On the other hand, the mRNA level of DREB2A gene increases when plants are exposed to salt stress (e.g. 150-250 mM NaCl) or dehydration stress (e.g. dehydrated state). Therefore, Arabidopsis thaliana plants which have been exposed to such stress may also be used.

mRNA is prepared, for example, by exposing Arabidopsis thaliana plants grown on GM medium to the dehydration stress, low temperature stress or salt stress mentioned above and then freezing them with liquid nitrogen. Subsequently, conventional techniques for mRNA preparation may be used. For example, the frozen plant are ground in a mortar. From the resultant ground material, a crude RNA fraction is extracted by the glyoxal method, the guanidine thiocyanate-cesium chloride method, the lithium chloride-urea method, the proteinase K-deoxyribonuclease method or the like. From this crude RNA fraction, poly(A)⁺ RNA (mRNA) can be obtained by the affinity column method using oligo dT-cellulose or poly U-Sepharose carried on Sepharose 2B or by the batch method. The resultant mRNA may further be fractionated by sucrose gradient centrifugation or the like.

Single-stranded cDNA is synthesized using the thus obtained mRNA as a template; this synthesis is performed using a commercial kit (e.g. ZAP-cDNA Synthesis Kit: Stratagene), oligo(dT)₂₀ and a reverse transcriptase. Then, double-stranded cDNA is synthesized from the resultant single-stranded cDNA. An appropriate adaptor such as EcoRI-NotI-BamHI adaptor is added to the resultant double-stranded cDNA, which is then ligated downstream of a transcriptional activation domain (such as GAL4 activation domain) in a plasmid (such as pAD-GAL4 plasmid: Stratagene) containing such a domain to thereby prepare a cDNA library.

1-2. A Host to Be Used in the Cloning of DREB Gene

DREB gene can be cloned, for example, by one hybrid screening method using yeast. Screening by this method may be performed using a commercial kit (e.g. Matchmaker One Hybrid System: Clontech).

In the cloning of DREB gene using the above-mentioned kit, first, it is necessary to ligate a DNA fragment comprising DRE sequences to which a protein encoded by DREB gene (i.e. DREB protein) binds to both plasmids pHISi-1 and pLacZi contained in the kit. Then, the resultant plasmids are transformed into the yeast contained in the kit (Saccharomyces cerevisiae YM4271) to thereby prepare a host yeast for cloning.

The host yeast for cloning can biosynthesize histidine by the action of HIS3 protein which is expressed leakily by HIS3 minimum promoter. Thus, usually, this yeast can grow in the absence of histidine. However, since the promoter used for the expression of the gene encoding HIS3 protein is a minimum promoter which can only maintain the minimum transcription level, HIS3 protein produced in cells is extremely small in quantity. Therefore, when the host yeast is cultured in the presence of 3-AT (3-aminotriazole) that is a competitive inhibitor against HIS3 protein, the function of HIS3 protein in cells is inhibited by 3-AT in a concentration dependent manner. When the concentration of 3-AT exceeds a specific level, HIS3 protein in cells becomes unable to function and, as a result, the host yeast becomes unable to grow in the absence of histidine. Similarly, lacZ gene is also located downstream of CYC1 minimum promoter. Thus, β -galactosidase is produced only in extremely small quantity in the yeast cells. Therefore, when the host yeast is plated on an Xgal containing plate, colonies appearing thereon do not have such Xgal degrading ability that turns the colonies into blue as a whole. However, when a transcription factor that binds to DRE sequences located upstream of HIS3 and lacZ genes and activate the transcription thereof is expressed in the host yeast, the yeast

becomes viable in the presence of a sufficient amount of 3-AT and, at the same time, Xgal is degraded to turn the colonies into blue.

As used herein, the term "dehydration responsive element (DRE)" refers to a cis-acting DNA domain consisting of a 9 bp conserved sequence 5'-TACCGACAT-3' located upstream of those genes which are expressed upon exposure to dehydration stress, low temperature stress, etc.

A DNA fragment comprising DRE can be obtained by amplifying the promoter region of rd29A gene (from -215 to -145 based on the translation initiation site of the gene) by polymerase chain reaction (PCR), rd29 gene being one of dehydration tolerance genes [Kazuko Yamaguchi-Shinozaki and Kazuo Shinozaki, The Plant Cell 6:251-264 (1994)]. As a template DNA which can be used in this PCR, genomic DNA from Arabidopsis thaliana is given. As a sense primer, 5'-aagcttaagcttacatcagttgaaagaaa-3' (SEQ ID NO: 11) may be used. As an antisense primer, 5'-aagcttaagcttgctttggaaactcatgtc-3' (SEQ ID NO: 12) may be used. Other primers may also be used in the present invention.

1-3. Cloning of DREB1A Gene and DREB2A Gene

DREB1A gene and DREB2A gene can be obtained by transforming the cDNA library obtained in subsection 1-1 above into the host obtained in subsection 1-2 above by the lithium acetate method or the like, plating the resultant transformant on LB medium plate or the like containing Xgal (5-bromo-4-chloro-3-indolyl- β -D-galactoside) and 3-AT (3-aminotriazole), culturing the transformant, selecting blue colonies appearing on the plate and isolating the plasmids therefrom.

Briefly, a positive clone containing DREB1A gene or DREB2A gene

contains a fusion gene composed of a DNA region coding for GAL4 activation domain (GAL4 AD) and a DNA region coding for a DRE-binding protein, and expresses a fusion protein (hybrid protein) composed of the DRE-binding protein and GAL4 activation domain under the control of alcohol dehydrogenase promoter. Subsequently, the expressed fusion protein binds, through the DRE-binding protein moiety, to DRE located upstream of a reporter gene. Then, GAL4 activation domain activates the transcription of lacZ gene and HIS3 gene. As a result, the positive clone produces remarkable amounts of HIS3 protein and β -galactosidase. Thus, because of the action of the HIS3 protein produced, the positive clone can biosynthesize histidine even in the presence of 3-AT. Therefore, the clone becomes viable in the presence of 3-AT and, at the same time, the Xgal in the medium is degraded by the β -galactosidase produced to turn the colonies into blue.

Subsequently, such blue colonies are subjected to single cell isolation, and the isolated cells are cultured. Then, plasmid DNA is purified from the cultured cells to thereby obtain DREB1A gene or DREB2A gene.

1-4. Homologues to DREB1A Protein or DREB2A Protein

Organisms may have a plurality of genes with similar nucleotide sequences which are considered to have evolved from a single gene. Proteins encoded by such genes are mutually called homologues. They can be cloned from the relevant gene library using as a probe a part of the gene of which the nucleotide sequence has already been known. In the present invention, genes encoding homologues to DREB1A or DREB2A protein can be cloned from the Arabidopsis thaliana cDNA library using DREB1A cDNA or DREB2A cDNA obtained in subsection 1-3

above as a probe.

1-5. Determination of Nucleotide Sequences

The cDNA portion is cut out from the plasmid obtained in subsection 1-3 or 1-4 above using a restriction enzyme and ligated to an appropriate plasmid such as pSK (Stratagene) for sub-cloning. Then, the entire nucleotide sequence is determined. Sequencing can be performed by conventional methods such as the chemical modification method by Maxam-Gilbert or the dideoxynucleotide chain termination method using M13 phage. Usually, sequencing is carried out with an automated DNA sequencer (e.g. Perkin-Elmer Model 373A DNA Sequencer).

SEQ ID NO: 1 shows the nucleotide sequence of DREB1A gene, and SEQ ID NO: 2 the amino acid sequence of the protein encoded by this gene. SEQ ID NO: 3 shows the nucleotide sequence of DREB2A gene, and SEQ ID NO: 4 the amino acid sequence of the protein encoded by this gene. SEQ ID NO: 5 shows the nucleotide sequence of DREB1B gene, and SEQ ID NO: 6 the amino acid sequence of the protein encoded by this gene. SEQ ID NO: 7 shows the nucleotide sequence of DREB1C gene, and SEQ ID NO: 8 the amino acid sequence of the protein encoded by this gene. SEQ ID NO: 9 shows the nucleotide sequence of DREB2B gene, and SEQ ID NO: 10 the amino acid sequence of the protein encoded by this gene. As long as a protein consisting of one of the above-mentioned amino acid sequences has a function to bind to DRE to thereby activate the transcription of genes located downstream of DRE, the amino acid sequence may have mutation (such as deletion, substitution or addition) in at least one amino acid. A mutated gene coding for the protein having such mutated amino acid sequence may also be used

in the present invention.

For example, at least 1 amino acid, preferably 1 to about 20 amino acids, more preferably 1 to 5 amino acids may be deleted in the amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8 or 10; at least 1 amino acid, preferably 1 to about 20 amino acids, more preferably 1 to 5 amino acids may be added to the amino acid sequence shown in SEQ ID NO: 2, 4, 8 or 10; or at least 1 amino acid, preferably 1 to about 160 amino acids, more preferably 1 to 40 amino acids may be substituted with other amino acid(s) in the amino acid sequence shown in SEQ ID NO: 2, 4, 8 or 10. A gene coding for a protein having such mutated amino acid sequence may be used in the present invention as long as the protein has a function to bind to DRE to thereby activate the transcription of genes located downstream of DRE.

Also, a DNA which can hybridize with the above-mentioned gene under stringent conditions may be used in the present invention as long as the protein encoded by the DNA has a function to bind to DRE to thereby activate the transcription of genes located downstream of DRE. The "stringent conditions" means, for example, those conditions in which formamide concentration is 30-50%, preferably 50%, and temperature is 37-50 °C, preferably 42°C.

A mutated gene may be prepared by known techniques such as the method of Kunkel, the gapped duplex method or variations thereof using a mutation introducing kit [e.g. Mutant-K (Takara) or Mutant-G (Takara)] or using LA PCR in vitro Mutagenesis Series Kit (Takara).

Once the nucleotide sequence of DREB gene has been determined definitely, the gene can be obtained by chemical synthesis, by PCR using the cDNA or genomic DNA of the gene as a template, or by

hybridization with a DNA fragment having the above nucleotide sequence as a probe.

The recombinant vectors containing DREB1A gene and DREB2A gene, respectively, were introduced into *E. coli* K-12 strain and deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology (1-3, Higashi 1-Chome, Tsukuba City, Ibaraki, Japan) under accession numbers FERM BP-6654 (*E. coli* containing DREB1A gene) and FERM BP-6655 (*E. coli* containing DREB2A gene) on August 11, 1998.

2. Determination of the DRE Binding Ability and Transcription

Activating Ability of the Proteins encoded by DREB Genes

2-1. Analysis of the DRE Binding Ability of the Proteins encoded by DREB Genes

The ability of the protein encoded by DREB gene (hereinafter referred to as the "DREB protein") to bind to DRE can be confirmed by performing a gel shift assay [Urao, T. et al., *The Plant Cell* 5:1529-1539 (1993)] using a fusion protein composed of the above protein and GST. A fusion protein composed of DREB1A protein and GST can be prepared as follows. First, DREB1A gene is ligated downstream of the GST coding region of a plasmid containing GST gene (e.g. pGEX-4T-1 vector: Pharmacia) so that the reading frames of the two genes coincide with each other. The resultant plasmid is transformed into *E. coli*, which is cultured under conditions that induce synthesis of the fusion protein. The resultant *E. coli* cells are disrupted by sonication, for example. Cell debris is removed from the disrupted material by centrifugation. Then, the supernatant is purified by

affinity chromatography using a carrier such as glutathione-Sepharose to thereby obtain the fusion protein.

Gel shift assay is a method for examining the interaction between a DNA and a protein. Briefly, a DRE-containing DNA fragment labelled with ^{32}P or the like is mixed with the fusion protein described above and incubated. The resultant mixture is electrophoresed. After drying, the gel is autoradiographed to detect those bands which have migrated behind as a result of the binding of the DNA fragment and the protein. In the present invention, the specific binding of DREB1A or DREB2A protein to the DRE sequence can be confirmed by making it clear that the above-mentioned behind band is not detected when a DNA fragment containing a varied DRE sequence is used.

2-2. Analysis of the Transcription Activating Ability of the Proteins Encoded by DREB Genes

The transcription activating ability of the proteins encoded by DREB genes can be analyzed by a trans-activation experiment using a protoplast system from Arabidopsis thaliana. For example, DREB1A cDNA is ligated to pBI221 plasmid (Clontech) containing CaMV35S promoter to construct an effector plasmid. On the other hand, 3 cassettes of the DRE-containing 71 base DNA region obtained in subsection 1-2 above are connected tandemly to prepare a DNA fragment, which is then ligated upstream of TATA promoter located upstream of β -glucuronidase (GUS) gene in pBI221 plasmid to construct a reporter plasmid. Subsequently, these two plasmids are introduced into protoplasts of Arabidopsis thaliana and then GUS activity is determined. If GUS activity is increased by the simultaneous expression of DREB1A protein, it is understood that DREB1A protein

expressed in the protoplasts is activating the transcription of GUS gene through the DRE sequence.

In the present invention, preparation of protoplasts and introduction of plasmid DNA into the protoplasts may be performed by the method of Abel et al. [Abel, S. et al., Plant J. 5:421-427 (1994)].

In order to minimize experimental errors resulted from the difference in plasmid DNA introduction efficiency by experiment, a plasmid in which luciferase gene is ligated downstream of CaMV35S promoter may be introduced into protoplasts together with the two plasmids described above, and β -glucuronidase activity against luciferase activity may be determined. Then, the determined value may be taken as a value indicating the transcription activating ability. β -glucuronidase activity can be determined by the method of Jefferson et al. [Jefferson, R.A. et al., EMBO J. 83:8447-8451 (1986)]; and luciferase activity can be determined using PicaGene Luciferase Assay Kit (Toyo Ink).

3. Creation of Transgenic Plants

A transgenic plant having tolerance to environmental stresses, in particular, low temperature stress (including freezing stress), dehydration stress and salt stress, can be created by introducing the gene obtained in section 1 above into a host plant using recombinant techniques. As a method for introducing the gene into a host plant, indirect introduction such as the Agrobacterium infection method, or direct introduction such as the particle gun method, polyethylene glycol method, liposome method, microinjection or the like may be used. When the Agrobacterium infection method is used, a transgenic plant can be created by the following procedures.

3-1. Preparation of a Recombinant Vector to be Introduced into a Plant and Transformation of Agrobacterium

A recombinant vector to be introduced into a plant can be prepared by digesting with an appropriate restriction enzyme a DNA comprising DREB1A, DREB1B, DREB1C, DREB2A or DREB2B gene obtained in section 1 above, ligating an appropriate linker to the resultant DNA if necessary, and inserting the DNA into a cloning vector for plant cells. As the cloning vector, a binary vector type plasmid such as pBI2113Not, pBI2113, pBI101, pBI121, pGA482, pGAH, pBIG; or an intermediate vector type plasmid such as pLGV23Neo, pNCAT, pMON200 may be used.

When a binary vector type plasmid is used, the gene of interest is inserted between the border sequences (LB, RB) of the binary vector. The resultant recombinant vector is amplified in *E. coli*. The amplified recombinant vector is introduced into Agrobacterium tumefaciens C58, LBA4404, EHA101, C58C1Rif^R, EHA105, etc. by freeze-thawing, electroporation or the like. The resultant Agrobacterium tumefaciens is used for the transduction of a plant of interest.

In addition to the method described above, the three-member conjugation method [Nucleic Acids Research, 12:8711 (1984)] may also be used to prepare DREB gene-containing Agrobacterium for use in plant infection. Briefly, an *E. coli* containing a plasmid comprising the gene of interest, an *E. coli* containing a helper plasmid (e.g. pRK2013) and an Agrobacterium are mixed and cultured on a medium containing rifampicin and kanamycin. Thus, a zygote Agrobacterium for use in plant infection can be obtained.

Since DREB gene encodes a protein which activates transcription, various genes are activated by the action of the expressed DREB

protein in a DREB gene-introduced plant. This leads to increase in energy consumption and activation of metabolism in the plant. As a result, the growth of the plant itself may be inhibited. As a means to prevent such inhibition, it is considered to ligate a stress responsive promoter upstream of DREB gene so that the DREB gene is expressed only when a stress is loaded. Specific examples of such a promoter include the following ones:

rd29A gene promoter [Yamaguchi-Shinozaki, K. et al., The Plant Cell 6:251-264 (1994)]

rd29B gene promoter [Yamaguchi-Shinozaki, K. et al., The Plant Cell 6:251-264 (1994)]

rd17 gene promoter [Iwasaki, T. et al., Plant Physiol., 115:1287 (1997)]

rd22 gene promoter [Iwasaki, T. et al., Mol. Gen. Genet., 247:391-398 (1995)]

DREB1A gene promoter [Shinwari, Z.K. et al., Biochem. Biophys. Res. Com. 250:161-170 (1988)]

cor6.6 gene promoter [Wang, H. et al., Plant Mol. Biol. 28:619-634 (1995)]

cor15a gene promoter [Baker, S.S. et al., Plant Mol. Biol. 24:701-713 (1994)]

erdl gene promoter [Nakashima K. et al., Plant J. 12:851-861 (1997)]

kin1 gene promoter [Wang, H. et al., Plant Mol. Biol. 28:605-617 (1995)]

Other promoter may also be used as long as it is known to be stress responsive and to function in plant. These promoters can be

obtained by PCR amplification using primers designed based on a DNA comprising the promoter and using relevant genomic DNA as a template.

If necessary, it is also possible to ligate a terminator which demands termination of transcription downstream of DREB gene. As the terminator, cauliflower mosaic virus-derived terminator or nopaline synthase gene terminator may be used. Other terminator may also be used as long as it is known to function in plant.

If necessary, an intron sequence which enhances the expression of a gene may be located between the promoter sequence and DREB gene. For example, the intron from maize alcohol dehydrogenase (Adh1) [Genes & Development 1:1183-1200 (1987)] may be introduced.

In order to select transformed cells of interest efficiently, it is preferable to use an effective selection marker gene in combination with DREB gene. As the selection marker, one or more genes selected from kanamycin resistance gene (NPTII), hygromycin phosphotransferase gene (htp) which confers resistance to the antibiotic hygromycin on plants, phosphinothricin acetyl transferase gene (bar) which confers resistance to bialaphos and the like.

DREB gene and the selection marker gene may be incorporated together into a single vector. Alternatively, the two genes may be incorporated into separate vectors to prepare two recombinant DNAs.

3-2. Introduction of DREB Gene into a Host Plant

In the present invention, the term "host plant" means any of the following: cultured plant cells, the entire plant of a cultured plant, plant organs (such as leaves, petals, stems, roots, rhizomes, seeds), or plant tissues (such as epidermis, phloem, parenchyma, xylem, vascular bundle). Specific examples of plants which may be used as a

host include Arabidopsis thaliana, tobacco, rice and maize.

DREB gene can be introduced into the above-described host plant by introducing a DREB gene-containing vector into plant sections by the Agrobacterium infection method, particle gun method or polyethylene glycol method. Alternatively, a DREB gene-containing vector may be introduced to protoplasts by electroporation.

If a gene of interest is introduced by the Agrobacterium infection method, a step of infecting a host plant with an Agrobacterium containing a plasmid comprising the gene of interest is necessary. This step can be performed by the vacuum infiltration method [CR Acad. Sci. Paris, Life Science, 316:1194 (1993)]. Briefly, Arabidopsis thaliana is grown in a soil composed of vermiculite and perlite (50:50). The resultant plant is dipped directly in a culture fluid of an Agrobacterium containing a plasmid comprising DREB gene, placed in a desiccator and then sucked with a vacuum pump to 65-70 mmHg. Then, the plant was allowed to stand at room temperature for 5-10 min. The plant pot is transferred to a tray and covered with a wrap to maintain the humidity. The next day, the wrap is removed. The plant is grown in that state to harvest seeds.

Subsequently, in order to select those individuals which have the gene of interest, seeds from various plant bodies are sown on MS agar medium supplemented with appropriate antibiotics. Arabidopsis thaliana grown on this medium are transferred to pots and grown there. As a result, seeds of a transgenic plant into which DREB gene is introduced can be obtained.

Generally, a transgene is located on the genome of the host plant. However, due to the difference in the locations on the genome, the expression of the transgene varies among transformants, presenting a

phenomenon called position effect. Those transformants in which the transgene is expressed more highly can be selected by assaying mRNA levels in transformants by Northern blot analysis using a DNA fragment from the transgene as a probe.

The confirmation that the gene of interest is integrated in the transgenic plant of the invention and in the subsequent generation thereof can be made by extracting DNA from cells and tissues of those plants by conventional methods and detecting the transgene by PCR or Southern analysis known in the art.

3-3. Analysis of Expression Levels and Expression Sites of DREB Gene in Plant Tissues

Expression levels and expression sites of DREB gene in a transgenic plant into which the gene is introduced can be analysed by extracting RNA from cells and tissues of the plant by conventional methods and detecting the mRNA of DREB gene by RT-PCR or Northern blot analysis known in the art. Alternatively, DREB protein may be analysed directly by Western blotting or the like using an antibody raised against the protein.

3-4. Changes in mRNA Levels of Various Genes in a Transgenic Plant in to which DREB Gene is Introduced

It is possible to identify by Northern blot analysis those genes whose expression levels are believed to have been changed as a result of the action of DREB protein in a transgenic plant into which DREB gene is introduced. Northern blotting can assay those genes by comparing their mRNA levels in the transgenic plant into which DREB gene is introduced and in plants into which the gene is not

introduced.

For example, plants grown on GM agar medium or the like are given dehydration and/or low temperature stress for a specific period of time (e.g. 1 to 2 weeks). Dehydration stress may be given by pulling out the plant from the agar medium and drying it on a filter paper for 10 min to 24 hr. Low temperature stress may be given by retaining the plant at 15 to -4 °C for 10 min to 24 hr. Total RNA is prepared from control plants which did not receive any stress and plants which received dehydration and low temperature stresses. The resultant total RNA is subjected to electrophoresis. Then, genes expressing are assayed by Northern blot analysis or RT-PCR.

3-5. Evaluation of the Tolerance to Environmental Stresses of the Transgenic Plant

The tolerance to environmental stresses of the transgenic plant into which DREB gene is introduced can be evaluated by setting the plant in a pot containing a soil comprising vermiculite, perlite and the like exposing the plant to various stresses such as dehydration, low temperature and freezing, and examining the survival of the plant. For example, tolerance to dehydration stress can be evaluated by leaving the plant without giving water for 2 to 4 weeks and then examining the survival. Tolerance to freezing stress can be evaluated by leaving the plant at -6 to -10 °C for 5 to 10 days, growing it at 20 to 25 °C for 5 to 10 days and then examining its survival ratio.

PREFERRED EMBODIMENTS OF THE INVENTION

Hereinbelow, the present invention will be described more

specifically with reference to the following Examples. However, the technical scope of the present invention is not limited to these Examples.

EXAMPLE 1

Cloning of DREB1A Gene and DREB2A Gene

(1) Cultivation of Arabidopsis thaliana Plant

Arabidopsis thaliana seeds obtained from LEHLE SEEDS were sterilized in a solution containing 1% sodium hypochlorite and 0.02% Triton X-100 for 15 min. After rinsing with sterilized water, 40-120 seeds were sown on GM agar medium [4.6 g/L mixed salts for Murashige-Skoog medium (Nihon Pharmaceutical Co., Ltd.), 0.5 g/L MES, 30 g/L sucrose, 8 g/L agar, pH 5.7] and cultured at 22 °C under conditions of 16 hr light (about 1000 lux) 8 hr dark, to thereby obtain plant.

(2) Preparation of Poly(A)⁺ RNA

The plant bodies obtained in (1) above were subjected to low temperature treatment at 4 °C for 24 hr, and then total RNA was prepared from them by the glyoxal method. Briefly, 3 g of Arabidopsis thaliana plant frozen in liquid nitrogen was suspended in 100 ml of 5.5 M GTC solution (5.5 M guanidine thiocyanate, 25 mM sodium citrate, 0.5% sodium N-lauroyl sarcosinate) and solubilized quickly with a homogenizer. This homogenate was sucked into and extruded from a syringe provided with a 18-G needle repeatedly more than 10 times to thereby disrupt the DNA. Then, the homogenate was centrifuged at 4°C at 12,000xg for 15 min to precipitate and remove the cell debris.

The resultant supernatant was overlayed on 17 ml of CsTFA solution [a solution obtained by mixing cesium trifluoroacetate

(Pharmacia), 0.25 M EDTA and sterilized water to give D=1.51] placed in an autoclaved centrifuge tube, and then ultracentrifuged in Beckmann SW28 Rotor at 15°C at 25,000 rpm for 24 hr to precipitate RNA.

The resultant RNA was dissolved in 600 μ l of 4 M GTC solution (obtained by diluting the above-described 5.5 M GTC solution with sterilized water to give a GTC concentration of 4 M) and precipitated with ethanol to thereby obtain total RNA of interest.

The resultant total RNA was dissolved in 2 ml of TE/NaCl solution (1:1 mixture of TE and 1 M NaCl) and passed through an oligo-dT cellulose column [prepared by packing a Bio-Rad Econocolumn (0.6 cm in diameter) with oligo-dT cellulose (type 3) (Collaborative Research) to a height of 1.5 cm] equilibrated with TE/NaCl in advance. The solution passed through the column was fed to the column again. Subsequently, the column was washed with about 8 ml of TE/NaCl. TE was added thereto to elute and purify poly(A)⁺ RNA. The amount of the thus obtained RNA was determined with a UV spectroscope.

(3) Synthesis of a cDNA Library

Double-stranded cDNA was synthesized with a cDNA synthesis kit (Stratagene) using 5 μ g of the poly(A)⁺ RNA obtained in (2) above. Then, the double-stranded cDNA was ligated to pAD-GAL4 plasmid (Stratagene) to thereby synthesize a cDNA library. Briefly, at first, single-stranded cDNA was synthesized in the following reaction solution according to the protocol attached to the kit.

Poly(A) ⁺ RNA	5 μ l (5 μ g)
10x 1st Strand synthesis buffer	5 μ l
DEPC-treated water	34 μ l
40 U/ μ l Ribonuclease inhibitor	1 μ l
Nucleotide mix for 1st strand	3 μ l
<u>1.4 μg/μl Linker primer</u>	<u>2 μl</u>
Total	50 μ l

To the above solution, 1.5 μ l (50 U/ μ l) of reverse transcriptase was added and incubated at 37 °C for 1 hr to thereby synthesize single-stranded cDNA. To the resultant reaction solution containing single-stranded cDNA, the following reagents were added in the indicated order.

Reaction solution containing single-stranded cDNA	45 μ l
10x 2nd Strand synthesis buffer	20 μ l
NTP mix for 2nd strand	6 μ l
1.5 U/ μ l RNase H	2 μ l
9 U/ μ l DNA polymerase I	11 μ l
<u>DEPC-treated water</u>	<u>116 μl</u>
Total	200 μ l

The resultant reaction solution was incubated at 16°C for 2.5 hr to thereby synthesize double-stranded cDNA.

The resultant double-stranded cDNA was blunt-ended by incubating it with 5 units of Pfu DNA polymerase at 72 °C for 30 min. Subsequently, the resultant cDNA was subjected to phenol/chloroform

extraction and ethanol precipitation. To the resultant pellet, 9 μ l of EcoRI-NotI-BamHI adaptor (Takara), 1 μ l of 10x ligase buffer, 1 μ l of ATP and 1 μ l of T4 DNA ligase (4 U/ μ l) were added and incubated at 4°C for 2 days to thereby add the adaptor to the double-stranded cDNA.

Subsequently, the cDNA having an EcoRI restriction enzyme site at both ends was ligated to the EcoRI site downstream of the GAL4 activation domain of pAD-GAL4 plasmid (Stratagene) (a cloning vector) with T4 DNA ligase to thereby synthesize a cDNA library.

(4) Preparation of Genomic DNA

Genomic DNA was prepared from the plant obtained in (1) above according to the method described by Maniatis, T. et al. [Molecular Cloning: A Laboratory Manual, pp. 187-198, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1982)]. Briefly, 2,000 ml of disruption buffer [0.35 M sucrose, 1 M Tris-HCl (pH 8.0), 5 mM MgCl₂, 50 mM KCl] was added to 50 g of Arabidopsis thaliana plant. The mixture was disrupted in a whirling blender for 1 min 3 times to homogenize the plant bodies.

The disrupted material was filtered to remove the cell residue. The filtrate was dispersed into centrifuge tubes and centrifuged in a swing rotor at 3,000xg at 4 °C for 10 min at a low speed. The resultant supernatant was discarded. The precipitate was suspended in 30 ml of ice-cooled disruption buffer and then re-centrifuged at a low speed. The same procedures were repeated 3 times until the green precipitate turned into white.

The resultant white precipitate was suspended in 10 ml of ice-cooled TE. To this suspension, 10 ml of lysis solution (0.2 M Tris-

HCl (pH 8.0), 50 mM EDTA, 2% sodium N-lauroyl sarcosinate) was added. Then, 0.1 ml of proteinase K (10 mg/ml) was added thereto to digest nuclei. The resultant digest was subjected to phenol treatment and ethanol precipitation. The DNA fiber obtained by the precipitation was recovered by centrifugation at 3,000xg for 5 min and dissolved in 1 ml of TE to thereby obtain genomic DNA.

(5) Construction of a Host Yeast for Use in Yeast One Hybrid Screening

For the cloning of a gene encoding the transcription factor (DRE-binding protein) to be used in the invention, a host was constructed (Fig. 1). This host for cloning comprises two plasmids, one containing 4 cassettes of DRE motif-containing DNA upstream of HIS3 reporter gene and the other containing 4 cassettes of DRE motif-containing DNA upstream of lacZ reporter gene. Briefly, first, the promoter region of rd29A gene (the region from -215 to -145 based on the translation initiation point of rd29A gene) comprising DRE sequence to which the transcription factor to be used in the invention binds to was amplified by PCR. As a sense primer, 5'-aagcttaagcttacatcagttgaaa-3' (SEQ ID NO: 11) was synthesized. As an antisense primer, 5'-aagcttaagcttgcttttggactcatgtc-3' (SEQ ID NO: 12) was synthesized. To these primers, a HindIII restriction site was introduced to their 5' end so that PCR fragments can be ligated to a vector easily after amplification. These primers were synthesized chemically with a fully automated DNA synthesizer (Perkin-Elmer). A PCR was performed using these primers and the genomic DNA from (4) above as a template. The composition of the PCR reaction solution was as follows.

Genomic DNA solution	5 μ l (100 ng)
Sterilized water	37 μ l
10x PCR buffer [1.2 M Tris-HCl (pH 8.0), 100 mM KCl, 60 mM $(\text{NH}_4)_2\text{SO}_4$, 1% Triton X-100, 0.1 mg/ml BSA]	5 μ l
50 pmol/ μ l Sense primer	1 μ l (50 pmol)
50 pmol/ μ l Antisense primer	1 μ l (50 pmol)
<u>KOD DNA polymerase (KOD-101, TOYOBO)</u>	<u>1 μl (2.5 U)</u>
Total	50 μ l

After the above reaction solution was mixed thoroughly, 50 μ l of mineral oil was overlaid on it. The PCR was performed 25 cycles, one cycle consisting of thermal denaturation at 98°C for 15 sec, annealing at 65°C for 2 sec and extension at 74°C for 30 sec. After completion of the reaction, 50 μ l of chloroform was added to the reaction solution, and then the resultant mixture was centrifuged at 4 °C at 15,000 rpm for 15 min. The resultant upper layer was recovered into a fresh microtube, to which 100 μ l of ethanol was added and mixed well. The mixture was centrifuged at 4°C at 15,000 rpm for 15 min to pellet the PCR product.

The resultant PCR product was digested with HindIII and then ligated to the HindIII site of vector pSK to yield a recombinant plasmid. This plasmid was transformed into *E. coli*. From the transformant, plasmid DNA was prepared to determine the nucleotide sequence. By these procedures, a transformant comprising pSK with a DNA fragment containing 4 cassettes of DRE connected in the same direction was selected.

The DNA fragment containing 4 cassettes of DRE was cut out from pSK plasmid using EcoRI and HincII, and then ligated to the EcoRI-MluI site upstream of the HIS3 minimum promoter of a yeast expression vector pHISi-1 (Clontech). Likewise, the DRE-containing DNA fragment was cut out from pSK plasmid using EcoRI and HincII, and then ligated to the EcoRI-SalI site upstream of the lacZ minimum promoter of a yeast expression vector pLacZi (Clontech). The resultant two plasmids were transformed into Saccharomyces cerevisiae YM4271 (MAT_a, ura3-52, his3-200, ade2-101, lys2-801, leu2-3, 112, trp1-903) (Clontech) to thereby yield a host yeast to be used in yeast one hybrid screening (Fig. 1).

(6) Cloning of DREB1A Gene and DREB2A Gene

The host yeast prepared in (5) above was transformed with the cDNA library prepared in (3) above. The resultant yeast transformants (1.2×10^6) were cultured and screened as described previously. As a result, two positive clones were obtained. The cDNAs of these clones were cut out from pAD-GAL4 plasmid using EcoRI and then ligated to the EcoRI site of pSK plasmid to thereby obtain recombinant plasmids pSKDREB1A and pSKDREB2A.

(7) Determination of the Nucleotide Sequences

The entire nucleotide sequences for the cDNAs were determined using plasmids pSKDREB1A and pSKDREB2A. These plasmids were prepared with an automated plasmid preparation apparatus Model PI-100 (Kurabo). For the sequencing reaction, a reaction robot CATALYST 800 (Perkin Elmer) was used. For the DNA sequencing, Perkin Elmer Sequencer Model

373A was used. As a result, it was found that the cDNA from plasmid pSKDREB1A consists of 933 bp (SEQ ID NO: 1) and that only one open reading frame exists therein which encodes a protein consisting of 216 amino acid residues with a presumed molecular weight of about 24.2 kDa (SEQ ID NO: 2). On the other hand, it was found that the cDNA from plasmid pSKDREB2A consists of 1437 bp (SEQ ID NO: 3) and that only one open reading frame exists therein which encodes a protein consisting of 335 amino acid residues with a presumed molecular weight of about 37.7 kDa (SEQ ID NO: 4).

(8) Isolation of Genes Encoding Homologues to DREB1A or DREB2A Protein

Genes encoding homologues to the protein encoded by DREB1A or DREB2A gene obtained in (6) above were isolated. Briefly, genes encoding such homologues were isolated from Arabidopsis thaliana λ gt11 cDNA library using as a probe a double-stranded cDNA fragment comprising DREB1A or DREB2A gene according to the method described by Sambrook, J. et al., Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press, NY (1989). As genes encoding homologues to DREB1A protein, DREB1B gene and DREB1C gene were obtained; as a gene encoding a homologue to DREB2A protein, DREB2B gene was obtained. As a result of DNA sequencing, it was found that DREB1B gene (SEQ ID NO: 5) was identical with the gene called CBF1 [Stockinger, E.J. et al., Proc. Natl. Acad. Sci. USA 94:1035-1040 (1997)], but DREB1C gene (SEQ ID NO: 7) and DREB2B gene (SEQ ID NO: 9) were found to be novel.

From the analysis of the open reading frame of DREB1C gene, it was found that the gene product encoded by this gene is a protein

consisting of 216 amino acid residues with a molecular weight of about 24.3 kDa (SEQ ID NO: 8). Also, it was found that the gene product encoded by DREB2B gene is a protein consisting of 330 amino acid residues with a molecular weight of about 37.1 kDa (SEQ ID NO: 10).

EXAMPLE 2

Analysis of the DRE-Binding Ability of DREB1A and DREB2A Proteins

The ability of DREB1A and DREB2A proteins to bind to DRE was analyzed by preparing a fusion protein composed of glutathione-S-transferase (GST) and DREB1A or DREB2A protein using *E. coli* and then performing a gel shift assay. Briefly, the 429 bp DNA fragment from position 119 to position 547 of the nucleotide sequence of DREB1A cDNA or the 500 bp DNA fragment from position 167 to position 666 of the nucleotide sequence of DREB2A cDNA was amplified by PCR. Then, the amplified fragment was ligated to the EcoRI-SalI site of plasmid pGEX-4T-1 (Pharmacia). After the introduction of this plasmid into *E. coli* JM109, the resultant transformant was cultured in 200 ml of 2x YT medium (Molecular Cloning, (1982) Cold Spring Harbor Laboratory Press). To this culture, 1 mM isopropyl β -D-thiogalactoside which activates the promoter in plasmid pGEX-4T-1 was added to thereby induce the synthesis of a fusion protein of DREB1A (or DREB2A) and GST.

E. coli in which the fusion protein had been induced was suspended in 13 ml of buffer (10 mM Tris-HCl, 0.1 mM DTT, 0.1 mM phenylmethylsulfonyl fluoride). Then, 1% Triton X-100 and 1 mM EDTA were added thereto. After the cells were disrupted by sonication, the disrupted material was centrifuged at 22,000xg for 20 min. Then, the

fusion protein of DREB1A (or DREB2A) and GST was purified by affinity chromatography using glutathione-Sepharose (Pharmacia) as a carrier. The resultant fusion protein was incubated with the DRE-containing 71 bp DNA fragment probe prepared by PCR and radiolabelled with ^{32}P at room temperature for 20 min. This mixture was electrophoresed using 6% acryl amide gel containing 0.25xTris-borate-EDTA at 100 V for 2 hr. Fig. 2 shows the results of autoradiogram on the gel after the electrophoresis. As is clear from this Figure, a band which migrated behind was detected when the fusion protein was incubated with the DRE-containing 71 bp DNA fragment probe (SEQ ID NO: 18). When a DNA fragment containing a varied DRE sequence (SEQ ID NO: 19, 20 or 21) was used, such a band was not detected. On the other hand, when a DNA fragment which was partly varied outside of DRE sequence (SEQ ID NO: 22 or 23) was used as a probe, a behind band was detected. Thus, it was shown that DREB1A or DREB2A protein specifically bound to DRE sequence.

EXAMPLE 3

Analysis of the Ability of DREB1A and DREB2A Proteins to Activate the Transcription of Genes Located Downstream of DRE

In order to examine whether DREB1A and DREB2A proteins are able to trans-activate DRE-dependent transcription in plant cells, a trans-activation experiment was conducted using a protoplast system prepared from *Arabidopsis thaliana* leaves. Briefly, the cDNA of DREB1A or DREB2A was ligated to a pBI221 plasmid containing CaMV35S promoter to thereby construct an effector plasmid. On the other hand, 3 cassettes of the DRE-containing 71 bp DNA region were connected tandemly to prepare a DNA fragment, which was then ligated upstream to

the minimum TATA promoter located upstream of β -glucuronidase (GUS) gene in a plasmid derived from pBI221 plasmid to construct a reporter plasmid. Subsequently, these two plasmids were introduced into protoplasts from *Arabidopsis thaliana* and then GUS activity was determined. When DREB1A or DREB2A protein was expressed simultaneously, GUS activity increased. This shows that DREB1A and DREB2A proteins are transcription factors which activate transcription through DRE sequence (Fig. 3).

EXAMPLE 4

Creation of a Transgenic Plant Containing a Gene in which a DNA
Encoding DREB1A Protein is Ligated
Downstream of CaMV35S Promoter

(1) Construction of a Plant Plasmid

Plasmid pSKDREB1A (10 μ g) obtained as described above was digested with EcoRV (20 U) and SmaI (20 U) in a buffer containing 10 mM Tris-HCl (pH 7.5), 10 mM MgCl₂, 1 mM dithiothreitol (DTT) and 100 mM NaCl at 37°C for 2 hr to thereby obtain a DNA fragment of about 0.9 kb containing DREB1A gene. On the other hand, plasmid pBI2113Not (10 μ g) containing promoter DNA was digested with SmaI in a buffer containing 10 mM Tris-HCl (pH 7.5), 10 mM MgCl₂, 1 mM DTT and 100 mM NaCl at 37 °C for 2 hr. The 0.9 kb DNA fragment containing DREB1A gene and the digested pBI2113Not were treated with T4 DNA ligase (2 U) in a buffer [66 mM Tris-HCl (pH 7.6), 6.6 mM MgCl₂, 10 mM DTT, 0.1 mM ATP] at 15 °C for 16 hr for ligation. The ligated DNA was transformed into *E. coli* JM109. The transformant was cultured, and plasmid pBI35S:DREB1A was obtained from the culture. Then, the nucleotide sequence was determined, and those plasmids in which

DREB1A gene was ligated in the sense direction were selected. Plasmid pBI2113Not mentioned above is a plasmid prepared by digesting pBI2113 [Plant Cell Physiology 37:49-59 (1996)] with SmaI and SacI to remove the coding region of GUS gene and ligating a SmaI-NotI-SacI polylinker to the resultant plasmid.

(2) Preparation of a Zygote Agrobacterium Containing the Plant Plasmid pBI35S:DREB1A

E. coli DH5 α containing the plant plasmid pBI35S:DREB1A prepared in (1) above, E. coli HB101 containing helper plasmid pRK2013 and Agrobacterium C58 were cultured in mixture on LB agar medium at 28 °C for 24 hr. Grown colonies were scraped off and suspended in 1 ml of LB medium. This suspension (10 ml) was plated on LB agar medium containing 100 μ g/ml rifampicin and 20 μ g/ml kanamycin and cultured at 28 °C for 2 days to thereby obtain a zygote Agrobacterium C58 (pBI35S:DREB1A).

(3) Gene Transfer into Arabidopsis thaliana by Agrobacterium Infection

The resultant zygote Agrobacterium was cultured in 10 ml of LB medium containing 100 μ g/ml rifampicin and 20 μ g/ml kanamycin at 28°C for 24 hr. Further, this culture fluid was added to 500 ml of LB medium and cultured for another 24 hr. The resultant culture fluid was centrifuged to remove the medium, and the cell pellet was suspended in 250 ml of LB medium.

On the other hand, 4 to 5 Arabidopsis thaliana plant bodies were grown in 9 cm pots containing soil composed of vermiculite and perlite (50:50) for 6 weeks. Then, the plant body was directly dipped

in the LB culture fluid of the Agrobacterium containing plasmid pBI35S:DREB1A and placed in a desiccator, which was sucked with a vacuum pump to reduce the pressure to 650 mmHg and then left for 10 min. Subsequently, the plant pot was transferred to a tray and covered with a wrap to maintain the humidity. The next day, the wrap was removed. Thereafter, the plant was grown uncovered to thereby obtain seeds. After sterilization in an aqueous solution of sodium hypochlorite, the seeds were sown on an agar medium for selection (MS medium supplemented with 100 μ g/ml vancomycin and 30 μ g/ml kanamycin). Arabidopsis thaliana seedlings grown on this medium were transplanted to pots and grown there to obtain seeds of the transformed plant.

(4) Identification of Genes Whose Expression Has Been Altered by the Transgene and the Transcription Factor Encoded by the Transgene

mRNA levels of those genes whose expression is considered to have been altered by the transgene DREB1A and the transcription factor encoded by this gene in the transformed plant were examined by Northern blot analysis. As a probe, a fragment of DREB1A, rd29A, kin1, cor6.6, cor15a, rd17, erd10, P5CS, erd1, rd22 or rd29B gene was used. In this Northern blot analysis, transformed and wild type Arabidopsis thaliana plants were used for comparing the expression of the above genes. Two grams each of plant bodies grown on GM agar medium for 3 weeks were exposed to dehydration stress and low temperature stress separately. Dehydration stress was given by pulling out the plant from the agar medium and drying it on a filter paper for 5 hr. Low temperature stress was given by retaining the plant at 4°C for 5 hr.

Total RNA was prepared separately from control plants which were given no stress, plants which were given dehydration stress and plants which were given low temperature stress. The resultant total RNA was subjected to electrophoresis. Then, expressing genes were assayed by Northern blot analysis. Generally, a transgene is located on the genome of a transformed plant in a similar manner. However, due to the difference in the locations on the genome, the expression of the transgene varies among transformants; this is a phenomenon called position effect. By assaying transformants by Northern blotting with a DNA fragment from the transgene as a probe, those transformants in which the transgene was expressed more highly were selected. Also, by using as a probe a DNA fragment of the above genes which are possibly involved in stress tolerance, those genes which exhibited changes in mRNA levels when DREB1A gene was introduced were identified (Fig. 5).

(5) Expression of Tolerance to Dehydration/Freezing Stress

Dehydration/freezing tolerance was investigated on Arabidopsis thaliana transformants which had been grown in 9 cm pots containing soil composed of vermiculite and perlite (50:50) for 3 weeks. As a control, Arabidopsis thaliana transformed with pBI121 not containing DREB1A gene was used. As to dehydration tolerance, water supply was stopped for 2 weeks and then plant survival was examined. As to freezing tolerance, the plant was maintained at -6°C for 2 days and then grown at 22°C for 5 days. Thereafter, its survival ratio was examined.

As a result, all the control plants were withered but the transgenic plants into which DREB1A gene was introduced exhibited a

high survival ratio (Fig. 6). However, inhibition of growth and dwarfing were observed in these transgenic plants.

EXAMPLE 5

Creation of a Transgenic Plant Containing
a Gene in which a DNA Encoding DREB1A Protein is Ligated
Downstream of rd29A Gene Promoter

(1) Construction of pBI29APNot Vector Containing rd29A Gene Promoter

An rd29A promoter region (from -861 to +63 based on the translation initiation point of rd29A gene) with HindIII site added to both ends was prepared by PCR under the same conditions as described in (4) in Example 2 using the following primers: 5'-aagcttaagcttgccatagatgcaattcaatc-3' (SEQ ID NO:13) and 5'-aagcttaagctttccaaagattttttctttccaa-3' (SEQ ID NO: 14). The resultant PCR fragment was digested with HindIII and inserted into the HindIII site of a plant binary vector pBI101 (Clontech, Palo Alto, CA, USA). β -glucuronidase gene (GUS) encoded in pBI101 was cut out with SmaI and SacI. Then, the resultant plasmid was ligated with SmaI-NotI-SacI polylinker. This plasmid was introduced into *E. coli* DH5a to prepare plasmid pBI29APNot.

(2) Construction of Plant Plasmid pBI29AP:DREB1A Using rd29A Gene Promoter

DREB1A gene was amplified by PCR using pSKDREB1A obtained in Example 1 as a template. Briefly, 5'-ggatccggatccatgaactcattttctgct-3' (SEQ ID NO: 15) was synthesized as a sense primer and 5'-ggatccggatcccttaataactccataacgata-3' (SEQ ID NO: 16) as an

antisense primer. BamHI site was introduced at 5' end of both primers so that the PCR fragment amplified can be ligated to the vector easily. The resultant PCR product was subjected to electrophoresis on 1% agarose gel. A band around 900-1000 bp was cut out from the gel. This gel fragment was placed in a fresh microtube, which was retained at 67 °C for 10 min to dissolve the gel. An equal volume of TE was added to the dissolved gel, mixed well and extracted with phenol. The resultant extract was centrifuged at 1,600xg for 3 min. Then, the aqueous layer was subjected to phenol extraction and phenol/chloroform extraction. To the resultant aqueous layer, cold ethanol was added to precipitate the PCR product.

The resultant PCR product (10 μ g) was dissolved in 30 μ l of TE and digested with BamHI (20 U). After heating at 70°C for 1 hr to deactivate BamHI, the digest was subjected to phenol extraction and ethanol precipitation to recover a DNA fragment containing DREB1A gene. Subsequently, this DNA fragment was ligated to the BamHI site of vector pBI29APNot. This recombinant plasmid was transformed into *E. coli* (DH5 α), and the transformant was selected by kanamycin resistance. The selected transformant was cultured in LB medium. Then the plasmid pBI29AP:DREB1A was extracted and purified from the transformant (Fig. 7).

(3) Preparation of a Zygote Agrobacterium Containing Plant Plasmid
pBI29AP:DREB1A

Using the recombinant plasmid pBI29AP:DREB1A obtained in (2) above, a zygote Agrobacterium containing plant plasmid pBI29AP:DREB1A was prepared in the same manner as in (2) in Example 5.

(4) Gene Transfer into Arabidopsis thaliana by Agrobacterium
Infection

Using the zygote Agrobacterium obtained in (3) above, plant plasmid pBI29AP:DREB1A was introduced into Arabidopsis thaliana in the same manner as in (3) in Example 5.

(5) Observation of the Growth and Dehydration/Freezing/Salt Stress
Tolerance of the Transformant

The transgenic Arabidopsis thaliana obtained in (4) above containing a plasmid in which DREB1A gene is ligated downstream of rd29A gene promoter, the transgenic Arabidopsis thaliana obtained in Example 5 containing a plasmid in which DREB1A gene is ligated downstream of CaMV35S gene promoter, and non-transformed Arabidopsis thaliana as a control were cultured under the same conditions. Then, their growth and survival ratios after the loading of dehydration, freezing or salt stress were examined. Briefly, each plant was planted in a 9 cm pot containing soil composed of vermiculite and perlite (50:50) and cultured outside. Figs. 8 and 9 present photographs showing the growth of plants on day 35 (Fig. 8A and Fig. 9A) and on day 65 (Fig. 8B and Fig. 9B) of the cultivation. In the pBI35S:DREB1A-introduced transgenic plant, a remarkable inhibition of growth was observed though there was some difference in the degree of growth among plants (Fig. 8A and Fig. 8B). In contrast, almost no inhibition of growth was observed in the pBI29AP:DREB1A-introduced transgenic plant (Fig. 9A and Fig. 9B).

Subsequently, their tolerance to stresses was examined. As to dehydration tolerance, water supply was stopped for 2 weeks and then plant survival was examined. As to freezing tolerance, plants were

maintained at -6 °C for 2 days and then grown at 22°C for 5 days. Thereafter, their survival ratios were examined. As to salt tolerance, plants were dipped in 600 mM NaCl for 2 hrs, then transferred to pots and grown there for 3 weeks. Thereafter, plant survival was examined. As a result, as shown in Fig. 10 and Tables 1 to 3, the control plants given dehydration or freezing stress were all withered. Only few control plants survived after the loading of salt stress. In the pBI35S:DREB1A-introduced transformant, the survival ratio varied among plants; those plants with higher expression of the introduced DREB1A gene exhibited higher tolerance. In contrast, in the pBI29AP:DREB1A-introduced transformant, the tolerance was almost equal among 43 plants analyzed. This transformant exhibited higher survival ratios than the pBI35S:DREB1A-introduced transformant. Thus, it was found that the transgenic plant created by the invention has high levels of tolerance to dehydration, freezing and salt, and yet exhibits good growth.

Table 1.

Survival Ratio of Transgenic Plants after the Loading of Freezing Stress

	No. of Individuals Survived	Total No. of Individuals	Survival Ratio (%)
rd29A:DREB1A	143	144	99.3
35S:DREB1Ab	47	56	83.9
35S:DREB1Ac	15	42	35.7
<u>Wild type</u>	0	55	0.0

Table 2.

Survival Ratio of Transgenic Plants after the Loading of Dehydration Stress

	No. of Individuals Survived	Total No. of Individuals	Survival Ratio(%)
rd29A:DREB1A	52	80	65.0
35S:DREB1Ab	15	35	42.9
35S:DREB1Ac	6	28	21.4
<u>Wild type</u>	0	25	0.0

Table 3.

Survival Ratio of Transgenic Plants after the Loading of Salt Stress

	No. of Individuals Survived	Total No. of Individuals	Survival Ratio(%)
rd29A:DREB1A	119	149	79.9
35S:DREB1Ab	4	24	16.7
<u>Wild type</u>	4	29	13.8

All publications, patents and patent applications cited herein are incorporated herein by reference in their entirety.

EFFECT OF THE INVENTION

According to the present invention, there is provided a transgenic plant containing a gene in which a DNA coding for a protein that binds to a stress responsive element and regulates the transcription of genes located downstream of the element is ligated downstream of a stress responsive promoter, the transgenic plant having improved tolerance to environmental stresses (such as dehydration, low temperature and salt) and being free from dwarfing.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DIRECTOR GENERAL OF JAPAN INTERNATIONAL RESEARCH CENTER FOR AGRICULTURAL SCIENCES, MINISTRY OF AGRICULTURE, FORESTRY AND FISHERIES -AND- BIO-ORIENTED TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION

(ii) TITLE OF INVENTION: ENVIRONMENT STRESS-TOLERANT PLANTS

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: SMART & BIGGAR

(B) STREET: P.O. BOX 2999, STATION D

(C) CITY: OTTAWA

(D) STATE: ONT

(E) COUNTRY: CANADA

(F) ZIP: K1P 5Y6

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

20 (D) SOFTWARE: ASCII (text)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: CA 2,269,105

(B) FILING DATE: 29-APR-1999

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 292348/1998

(B) FILING DATE: 14-OCT-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: SMART & BIGGAR

30 (B) REGISTRATION NUMBER:

(C) REFERENCE/DOCKET NUMBER: 72813-103

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (613)-232-2486

(B) TELEFAX: (613)-232-8440

(2) INFORMATION FOR SEQ ID NO.: 1:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 933

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

10 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE

(A) NAME/KEY: CDS

(B) LOCATION: (119)..(766)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1:

CCTGAAC TAG AACAGAAAGA GAGAGAAACT ATTATTCAG CAAACCATA CAAACAAAAA 60

GACAGAGATC TTTAGTTAC CTTATCCAGT TTCTTGAAAC AGAGTACTCT TCTGATCA 118

20 ATG AAC TCA TTT TCT GCT TTT TCT GAA ATG TTT GGC TCC GAT TAC GAG 166
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu
1 5 10 15TCT TCG GTT TCC TCA GGC GGT GAT TAT ATT CCG ACG CTT GCG AGC AGC 214
Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser
20 25 30TGC CCC AAG AAA CCG GCG GGT CGT AAG AAG TTT CGT GAG ACT CGT CAC 262
Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
35 40 4530 CCA ATA TAC AGA GGA GTT CGT CGG AGA AAC TCC GGT AAG TGG GTT TGT 310
Pro Ile Tyr Arg Gly Val Arg Arg Asn Ser Gly Lys Trp Val Cys
50 55 60GAG GTT AGA GAA CCA AAC AAG AAA ACA AGG ATT TGG CTC GGA ACA TTT 358
Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
65 70 75 8040 CAA ACC GCT GAG ATG GCA GCT CGA GCT CAC GAC GTT GCC GCT TTA GCC 406
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
85 90 95CTT CGT GGC CGA TCA GCC TGT CTC AAT TTC GCT GAC TCG GCT TGG AGA 454
Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
100 105 110

CTC CCG ATC CCG GAA TCA ACT TGC GCT AAG GAC ATC CAA AAG GCG GCG	502
Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala	
115 120 125	
GCT GAA GCT GCG TTG GCG TTT CAG GAT GAG ATG TGT GAT GCG ACG ACG	550
Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr	
130 135 140	
GAT CAT GGC TTC GAC ATG GAG GAG ACG TTG GTG GAG GCT ATT TAC ACG	598
Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr	
145 150 155 160	
GCG GAA CAG AGC GAA AAT GCG TTT TAT ATG CAC GAT GAG GCG ATG TTT	646
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe	
165 170 175	
GAG ATG CCG AGT TTG TTG GCT AAT ATG GCA GAA GGG ATG CTT TTG CCG	694
Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro	
180 185 190	
20 CTT CCG TCC GTA CAG TGG AAT CAT AAT CAT GAA GTC GAC GGC GAT GAT	742
Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp	
195 200 205	
GAC GAC GTA TCG TTA TGG AGT TAT TAAAAACTCAG ATTATTATTT CCATTTTAG	796
Asp Asp Val Ser Leu Trp Ser Tyr	
210 215	
TACGATACTT TTTATTTAT TATTATTTT AGATCCTTTT TTAGAATGGA ATCTTCATTA	856
30 TGTTTGTAAA ACTGAGAAC GAGTGTAAAT TAAATTGATT CAGTTTCAGT ATAAAAAAAAA	916
AAAAAAAAAAA AAAAAAA	933

(2) INFORMATION FOR SEQ ID NO.: 2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 216

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

40 (ii) MOLECULE TYPE: polypeptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2:

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu	
1 5 10 15	

Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser	
20 25 30	

Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
 35 40 45

Pro Ile Tyr Arg Gly Val Arg Arg Asn Ser Gly Lys Trp Val Cys
 50 55 60

Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe
 65 70 75 80

10 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala
 85 90 95

Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg
 100 105 110

Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala
 115 120 125

20 Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr
 130 135 140

Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr
 145 150 155 160

Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe
 165 170 175

Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro
 180 185 190

30 Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp
 195 200 205

Asp Asp Val Ser Leu Trp Ser Tyr
 210 215

(2) INFORMATION FOR SEQ ID NO.: 3:

(i) SEQUENCE CHARACTERISTICS

40 (A) LENGTH: 1437

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE

(A) NAME/KEY: CDS

(B) LOCATION: (167)..(1171)

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 3:

GCTGTCTGAT AAAAGAAGA GGAAAACCG AAAAGCTAC ACACAAGAAG AGAAGAAAA 60
 GATACGAGCA AGAAGACTAA ACACGAAAGC GATTTATCAA CTCGAAGGAA GAGACTTGA 120
 TTTTCAAATT TCGTCCCCCTA TAGATTGTGT TGTTCTGGG AAGGAG ATG GCA GTT 175
 Met Ala Val
 1

TAT GAT CAG AGT GGA GAT AGA AAC AGA ACA CAA ATT GAT ACA TCG AGG 223
 Tyr Asp Gln Ser Gly Asp Arg Asn Arg Thr Gln Ile Asp Thr Ser Arg
 5 10 15

10 AAA AGG AAA TCT AGA AGT AGA GGT GAC GGT ACT ACT GTG GCT GAG AGA 271
 Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val Ala Glu Arg
 20 25 30 35

TTA AAG AGA TGG AAA GAG TAT AAC GAG ACC GTA GAA GAA GTT TCT ACC 319
 Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu Val Ser Thr
 40 45 50

20 AAG AAG AGG AAA GTA CCT GCG AAA GGG TCG AAG AAG GGT TGT ATG AAA 367
 Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys Met Lys
 55 60 65

GGT AAA GGA GGA CCA GAG AAT AGC CGA TGT AGT TTC AGA GGA GTT AGG 415
 Gly Lys Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg Gly Val Arg
 70 75 80

CAA AGG ATT TGG GGT AAA TGG GTT GCT GAG ATC AGA GAG CCT AAT CGA 463
 Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg
 85 90 95

30 GGT AGC AGG CTT TGG CTT GGT ACT TTC CCT ACT GCT CAA GAA GCT GCT 511
 Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln Glu Ala Ala
 100 105 110 115

TCT GCT TAT GAT GAG GCT GCT AAA GCT ATG TAT GGT CCT TTG GCT CGT 559
 Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro Leu Ala Arg
 120 125 130

40 CTT AAT TTC CCT CGG TCT GAT GCG TCT GAG GTT ACG AGT ACC TCA AGT 607
 Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser Thr Ser Ser
 135 140 145

CAG TCT GAG GTG TGT ACT GTT GAG ACT CCT GGT TGT GTT CAT GTG AAA 655
 Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val His Val Lys
 150 155 160

ACA GAG GAT CCA GAT TGT GAA TCT AAA CCC TTC TCC GGT GGA GTG GAG 703
 Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly Gly Val Glu
 165 170 175

50 CCG ATG TAT TGT CTG GAG AAT GGT GCG GAA GAG ATG AAG AGA GGT GTT 751
 Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys Arg Gly Val
 180 185 190 195

AAA GCG GAT AAG CAT TGG CTG AGC GAG TTT GAA CAT AAC TAT TGG AGT 799
 Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn Tyr Trp Ser
 200 205 210

60 GAT ATT CTG AAA GAG AAA GAG CAG AAG GAG CAA GGG ATT GTA GAA 847
 Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly Ile Val Glu
 215 220 225

ACC TGT CAG CAA CAA CAG CAG GAT TCG CTA TCT GTT GCA GAC TAT GGT	895
Thr Cys Gln Gln Gln Gln Asp Ser Leu Ser Val Ala Asp Tyr Gly	
230 235 240	
TGG CCC AAT GAT GTG GAT CAG AGT CAC TTG GAT TCT TCA GAC ATG TTT	943
Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser Asp Met Phe	
245 250 255	
GAT GTC GAT GAG CTT CTA CGT GAC CTA AAT GGC GAC GAT GTG TTT GCA	991
Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp Val Phe Ala	
10 260 265 270 275	
GGC TTA AAT CAG GAC CGG TAC CCG GGG AAC AGT GTT GCC AAC GGT TCA	1039
Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala Asn Gly Ser	
280 285 290	
TAC AGG CCC GAG AGT CAA CAA AGT GGT TTT GAT CCG CTA CAA AGC CTC	1087
Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu Gln Ser Leu	
295 300 305	
AAC TAC GGA ATA CCT CCG TTT CAG CTC GAG GGA AAG GAT GGT AAT GGA	1135
Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp Gly Asn Gly	
20 310 315 320	
TTC TTC GAC GAC TTG AGT TAC TTG GAT CTG GAG AAC TAAACAAAAAC	1181
Phe Phe Asp Asp Leu Ser Tyr Leu Asp Leu Glu Asn	
325 330 335	
AATATGAAGC TTTTGATT TGATATTGC CTTAATCCCA CAACGACTGT TGATTCTCTA	1241
30 TCCGAGTTT AGTGATATAG AGAACTACAG AACACGTTT TTCTTGTAT AAAGGTGAAC	1301
TGTATATATC GAAACAGTGA TATGACAATA GAGAAGACAA CTATAGTTG TTAGTCTGCT	1361
TCTCTTAAGT TGTTCTTAG ATATGTTTA TGTTTGTAA CAACAGGAAT GAATAATACA	1421
CACTTGTAAA AAAAAA	1437

(2) INFORMATION FOR SEQ ID NO.: 4:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 335
 - (B) TYPE: amino acid
- 40 (C) STRANDEDNESS:
 - (D) TOPOLOGY:
 - (ii) MOLECULE TYPE: polypeptide
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Arabidopsis thaliana*
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4:

Met Ala Val Tyr Asp Gln Ser Gly Asp Arg Asn Arg Thr Gln Ile Asp
 1 5 10 15

Thr Ser Arg Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val
 20 25 30

Ala Glu Arg Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu
 35 40 45

10 Val Ser Thr Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly
 50 55 60

Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg
 65 70 75 80

Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu
 85 90 95

20 Pro Asn Arg Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln
 100 105 110

Glu Ala Ala Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro
 115 120 125

Leu Ala Arg Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser
 130 135 140

Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val
 145 150 155 160

30 His Val Lys Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly
 165 170 175

Gly Val Glu Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys
 180 185 190

Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn
 195 200 205

40 Tyr Trp Ser Asp Ile Leu Lys Glu Lys Glu Lys Gln Lys Glu Gln Gly
 210 215 220

Ile Val Glu Thr Cys Gln Gln Gln Gln Asp Ser Leu Ser Val Ala
 225 230 235 240

Asp Tyr Gly Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser
 245 250 255

50 Asp Met Phe Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp
 260 265 270

Val Phe Ala Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala
 275 280 285

Asn Gly Ser Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu
 290 295 300

Gln Ser Leu Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp
 305 310 315 320

60 Gly Asn Gly Phe Phe Asp Asp Leu Ser Tyr Leu Asp Leu Glu Asn
 325 330 335

(2) INFORMATION FOR SEQ ID NO.: 5:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 937

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE

(A) NAME/KEY: CDS

(B) LOCATION: (164)...(802)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 5:

CTTGGAAAAG AATCTACCTG AAAAGAAAAA AAAGAGAGAG AGATATAAAAT AGCTTTACCA 60
 AGACAGATAT ACTATCTTT ATTAAATCCAA AAAGACTGAG AACTCTAGTA ACTACGTACT 120
 ACTTAAACCT TATCCAGTTT CTTGAAACAG AGTACTCTGA TCA ATG AAC TCA TTT 175
 Met Asn Ser Phe

1

20 TCA GCT TTT TCT GAA ATG TTT GGC TCC GAT TAC GAG CCT CAA GGC GGA 223
 Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu Pro Gln Gly Gly
 5 10 15 20

GAT TAT TGT CCG ACG TTG GCC ACG AGT TGT CCG AAG AAA CCG GCG GGC 271
 Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly
 25 30 35

30 CGT AAG AAG TTT CGT GAG ACT CGT CAC CCA ATT TAC AGA GGA GTT CGT 319
 Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg
 40 45 50

CAA AGA AAC TCC GGT AAG TGG GTT TCT GAA GTG AGA GAG CCA AAC AAG 367
 Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg Glu Pro Asn Lys
 55 60 65

AAA ACC AGG ATT TGG CTC GGG ACT TTC CAA ACC GCT GAG ATG GCA GCT 415
 Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala
 70 75 80

40 CGT GCT CAC GAC GTC GCT GCA TTA GCC CTC CGT GGC CGA TCA GCA TGT 463
 Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys
 85 90 95 100

CTC AAC TTC GCT GAC TCG GCT TGG CGG CTA CGA ATC CCG GAG TCA ACA 511
 Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr
 105 110 115

	TGC GCC AAG GAT ATC CAA AAA GCG GCT GCT GAA GCG GCG TTG GCT TTT Cys Ala Lys Asp Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Ala Phe 120 125 130	559
	CAA GAT GAG ACG TGT GAT ACG ACG ACC ACG AAT CAT GGC CTG GAC ATG Gln Asp Glu Thr Cys Asp Thr Thr Thr Asn His Gly Leu Asp Met 135 140 145	607
10	:GAG GAG ACG ATG GTG GAA GCT ATT TAT ACA CCG GAA CAG AGC GAA GGT Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Glu Gly 150 155 160	655
	GCG TTT TAT ATG GAT GAG GAG ACA ATG TTT GGG ATG CCG ACT TTG TTG Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met Pro Thr Leu Leu 165 170 175 180	703
	GAT AAT ATG GCT GAA GGC ATG CTT TTA CCG CCG CCG TCT GTT CAA TGG Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro Ser Val Gln Trp 185 190 195	751
20	AAT CAT AAT TAT GAC GGC GAA GGA GAT GGT GAC GTG TCG CTT TGG AGT Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val Ser Leu Trp Ser 200 205 210	799
	TAC TAATATTCGA TAGTCGTTTC CATTGGTGA CTATAGTTG AAAATATTCT Tyr	852
	AGTTCCCTTT TTTAGAATGG TTCCTTCATT TTATTTTATT TTATTGTTGT AGAAACGAGT	912
	GGAAAATAAT TCAATACAAA AAAAAA	937
30		

(2) INFORMATION FOR SEQ ID NO.: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 213

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: polypeptide

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 6:

Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu 1 5 10 15
--

Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys 20 25 30

Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr 35 40 45

Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg
 50 55 60
 Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala
 65 70 75 80
 Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly
 85 90 95
 10 Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile
 100 105 110
 Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Glu Ala
 115 120 125
 Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Asn His
 130 135 140
 20 Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu
 145 150 155 160
 Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met
 165 170 175
 Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro
 180 185 190
 Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val
 195 200 205
 30 Ser Leu Trp Ser Tyr
 210

(2) INFORMATION FOR SEQ ID NO.: 7:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 944

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

40 (D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE

(A) NAME/KEY: CDS

(B) LOCATION: (135)..(782)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 7:

CCTGAATTAG AAAAGAAAGA TAGATAGAGA AATAAATATT TTATCATACC ATACAAAAAA 60
 AGACAGAGAT CTTCTACTTA CTCTACTCTC ATAAACCTTA TCCAGTTCT TGAAACAGAG 120

	TACTCTTCTG ATCA ATG AAC TCA TTT TCT GCC TTT TCT GAA ATG TTT GGC	170
	Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly	
	1 5 10	
	TCC GAT TAC GAG TCT CCG GTT TCC TCA GGC GGT GAT TAC AGT CCG AAG	218
	Ser Asp Tyr Glu Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys	
	15 20 25	
10	CTT GCC ACG AGC TGC CCC AAG AAA CCA GCG GGA AGG AAG AAG TTT CGT	266
	Leu Ala Thr Ser Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg	
	30 35 40	
	GAG ACT CGT CAC CCA ATT TAC AGA GGA GTT CGT CAA AGA AAC TCC GGT	314
	Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly	
	45 50 55 60	
	AAG TGG GTG TGT GAG TTG AGA GAG CCA AAC AAG AAA ACG AGG ATT TGG	362
	Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp	
20	65 70 75	
	CTC GGG ACT TTC CAA ACC GCT GAG ATG GCA GCT CGT GCT CAC GAC GTC	410
	Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val	
	80 85 90	
	GCC GCC ATA GCT CTC CGT GGC AGA TCT GCC TGT CTC AAT TTC GCT GAC	458
	Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp	
	95 100 105	
30	TCG GCT TGG CGG CTA CGA ATC CCG GAA TCA ACC TGT GCC AAG GAA ATC	506
	Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile	
	110 115 120	
	CAA AAG GCG GCG GCT GAA GCC GCG TTG AAT TTT CAA GAT GAG ATG TGT	554
	Gln Lys Ala Ala Ala Glu Ala Leu Asn Phe Gln Asp Glu Met Cys	
	125 130 135 140	
	CAT ATG ACG ACG GAT GCT CAT GGT CTT GAC ATG GAG GAG ACC TTG GTG	602
	His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val	
	145 150 155	
40	GAG GCT ATT TAT ACG CCG GAA CAG AGC CAA GAT GCG TTT TAT ATG GAT	650
	Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp	
	160 165 170	
	GAA GAG GCG ATG TTG GGG ATG TCT AGT TTG TTG GAT AAC ATG GCC GAA	698
	Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu	
	175 180 185	
50	GGG ATG CTT TTA CCG TCG CCG TCG GTT CAA TGG AAC TAT AAT TTT GAT	746
	Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp	
	190 195 200	
	GTC GAG GGA GAT GAT GAC GTG TCC TTA TGG AGC TAT TAAAAATTCTGA	792
	Val Glu Gly Asp Asp Val Ser Leu Trp Ser Tyr	
	205 210 215	
	TTTTTATTTC CATTTCGGT ATTATAGCTT TTTATACATT TGATCCTTT TTAGAATGGA	852
	TCTTCTTCTT TTTTGGTTG TGAGAACGA ATGTAAATGG TAAAAGTTGT TGTCAAATGC	912
	AAATGTTTT GAGTGCAGAA TATATAATCT TT	944

(2) INFORMATION FOR SEQ ID NO.: 8:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 216

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: polypeptide

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 8:

Met	Asn	Ser	Phe	Ser	Ala	Phe	Ser	Glu	Met	Phe	Gly	Ser	Asp	Tyr	Glu
1									10						15

Ser	Pro	Val	Ser	Ser	Gly	Gly	Asp	Tyr	Ser	Pro	Lys	Leu	Ala	Thr	Ser
									25						30
20															

Cys	Pro	Lys	Lys	Pro	Ala	Gly	Arg	Lys	Lys	Phe	Arg	Glu	Thr	Arg	His
									40						45
35															

20 (A) ORGANISM: *Arabidopsis thaliana*

Pro	Ile	Tyr	Arg	Gly	Val	Arg	Gln	Arg	Asn	Ser	Gly	Lys	Trp	Val	Cys
									55						60
50															

Glu	Leu	Arg	Glu	Pro	Asn	Lys	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Phe
									75						80
65															

Gln	Thr	Ala	Glu	Met	Ala	Ala	Arg	Ala	His	Asp	Val	Ala	Ala	Ile	Ala
									85						95

30 (A) ORGANISM: *Arabidopsis thaliana*

Leu	Arg	Gly	Arg	Ser	Ala	Cys	Leu	Asn	Phe	Ala	Asp	Ser	Ala	Trp	Arg
									105						110
100															

Leu	Arg	Ile	Pro	Glu	Ser	Thr	Cys	Ala	Lys	Glu	Ile	Gln	Lys	Ala	Ala
									120						125
115															

Ala	Glu	Ala	Ala	Leu	Asn	Phe	Gln	Asp	Glu	Met	Cys	His	Met	Thr	Thr
									135						140
130															

40 (A) ORGANISM: *Arabidopsis thaliana*

Asp	Ala	His	Gly	Leu	Asp	Met	Glu	Glu	Thr	Leu	Val	Glu	Ala	Ile	Tyr
									155						160
145															

Thr	Pro	Glu	Gln	Ser	Gln	Asp	Ala	Phe	Tyr	Met	Asp	Glu	Glu	Ala	Met
									170						175
165															

50 (A) ORGANISM: *Arabidopsis thaliana*

Leu	Gly	Met	Ser	Ser	Leu	Leu	Asp	Asn	Met	Ala	Glu	Gly	Met	Leu	Leu
									185						190
180															

Pro	Ser	Pro	Ser	Val	Gln	Trp	Asn	Tyr	Asn	Phe	Asp	Val	Glu	Gly	Asp
									200						205
195															

Asp	Asp	Val	Ser	Leu	Trp	Ser	Tyr								
								215							
210															

(2) INFORMATION FOR SEQ ID NO.: 9:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1513

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(ix) FEATURE

(A) NAME/KEY: CDS

(B) LOCATION: (183)..(1172)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 9:

GAGACGCTAG	AAAGAACGCG	AAAGCTTGC	GAGAAGATT	GCTTTGATC	GA	CTTAACAC	60									
GAACAA	ACAAA	CAACATCTGC	GTGATAAAGA	AGAGATTTT	GCCTAAATAA	AGAAGAGATT	120									
CGACTCTAAT	CCTGGAGTTA	TCATT	CACGA	TAGATTCTTA	GATT	GCGACT	ATAAAGAAGA	180								
AG	ATG	GCT	GTA	TAT	GAA	CAA	ACC	66								
20	Met	Ala	Val	Tyr	Glu	Gln	Thr	Gly	227							
	1	5	10	15	15											
AAA	TCT	AGG	GCT	CGA	GCA	GGT	GGT	TTA	ACG	GTG	GCT	GAT	AGG	CTA	AAG	275
Lys	Ser	Arg	Ala	Arg	Ala	Gly	Gly	Leu	Thr	Val	Ala	Asp	Arg	Leu	Lys	
20	25	30														
AAG	TGG	AAA	GAG	TAC	AAC	GAG	ATT	GTT	GAA	GCT	TCG	GCT	GTT	AAA	GAA	323
Lys	Trp	Lys	Glu	Tyr	Asn	Glu	Ile	Val	Glu	Ala	Ser	Ala	Val	Lys	Glu	
35	40	45														
GGA	GAG	AAA	CCG	AAA	CGC	AAA	GTT	CCT	GCG	AAA	GGG	TCG	AAG	AAA	GGT	371
Gly	Glu	Lys	Pro	Lys	Arg	Lys	Val	Pro	Ala	Lys	Gly	Ser	Lys	Lys	Gly	
50	55	60														
TGT	ATG	AAG	GGT	AAA	GGA	GGA	CCA	GAT	AAT	TCT	CAC	TGT	AGT	TTT	AGA	419
Cys	Met	Lys	Gly	Lys	Gly	Gly	Pro	Asp	Asn	Ser	His	Cys	Ser	Phe	Arg	
65	70	75														
GGA	GTT	AGA	CAA	AGG	ATT	TGG	GGT	AAA	TGG	GTT	GCA	GAG	ATT	CGA	GAA	467
Gly	Val	Arg	Gln	Arg	Ile	Trp	Gly	Lys	Trp	Val	Ala	Glu	Ile	Arg	Glu	
80	85	90														
CCG	AAA	ATA	GGA	ACT	AGA	CTT	TGG	CTT	GGT	ACT	TTT	CCT	ACC	GCG	GAA	515
Pro	Lys	Ile	Gly	Thr	Arg	Leu	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Ala	Glu	
100	105	110														

	AAA GCT GCT TCC GCT TAT GAT GAA GCG GCT ACC GCT ATG TAC GGT TCA	563
	Lys Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser	
	115 120 125	
	TTG GCT CGT CTT AAC TTC CCT CAG TCT GTT GGG TCT GAG TTT ACT AGT	611
	Leu Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser	
	130 135 140	
10	ACG TCT AGT CAA TCT GAG GTG TGT ACG GTT GAA AAT AAG GCG GTT GTT	659
	Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val	
	145 150 155	
	TGT GGT GAT GTT TGT GTG AAG CAT GAA GAT ACT GAT TGT GAA TCT AAT	707
	Cys Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn	
	160 165 170 175	
	CCA TTT AGT CAG ATT TTA GAT GTT AGA GAA GAG TCT TGT GGA ACC AGG	755
	Pro Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg	
	180 185 190	
20	CCG GAC AGT TGC ACG GTT GGA CAT CAA GAT ATG AAT TCT TCG CTG AAT	803
	Pro Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn	
	195 200 205	
	TAC GAT TTG CTG TTA GAG TTT GAG CAG CAG TAT TGG GGC CAA GTT TTG	851
	Tyr Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu	
	210 215 220	
30	CAG GAG AAA GAG AAA CCG AAG CAG GAA GAA GAG GAG ATA CAG CAA CAG	899
	Gln Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Ile Gln Gln Gln	
	225 230 235	
	CAA CAG GAA CAG CAA CAG CAA CAG CTG CAA CCG GAT TTG CTT ACT GTT	947
	Gln Gln Glu Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val	
	240 245 250 255	
	GCA GAT TAC GGT TGG CCT TGG TCT AAT GAT ATT GTA AAT GAT CAG ACT	995
	Ala Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr	
	260 265 270	
40	TCT TGG GAT CCT AAT GAG TGC TTT GAT ATT AAT GAA CTC CTT GGA GAT	1043
	Ser Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp	
	275 280 285	
	TTG AAT GAA CCT GGT CCC CAT CAG AGC CAA GAC CAA AAC CAC GTA AAT	1091
	Leu Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn	
	290 295 300	
50	TCT GGT AGT TAT GAT TTG CAT CCG CTT CAT CTC GAG CCA CAC GAT GGT	1139
	Ser Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly	
	305 310 315	
	CAC GAG TTC AAT GGT TTG AGT TCT CTG GAT ATT TGAGAGTTCT GAGGCAATGG	1192
	His Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile	
	320 325 330	
	TCCTACAAGA CTACAACATA ATCTTGGAT TGATCATAGG AGAAACAAGA AATAGGTGTT	1252
	AATGATCTGA TTCACAATGA AAAAATATTT AATAACTCTA TAGTTTTGT TCTTCCTTG	1312
	GATCATGAAC TGTTGCTTCT CATCTATTGA GTTAATATAG CGAATAGCAG AGTTTCTCTC	1372
60	TTTCTTCTCT TTGTAGAAAA AAAAAAAA AAAAAAAA AAAAAAAAYH SAKMABGCAR	1432

SRCSDVSNAA NNTRNATNAR SARCHCNTRR AGRCTRASN CSRCASWASH TSKBABARAK 1492
 AANTAMAYSA KMASRNGNGA C 1513

(2) INFORMATION FOR SEQ ID NO.: 10:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 330

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY:

(ii) MOLECULE TYPE: polypeptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 10:

Met	Ala	Val	Tyr	Glu	Gln	Thr	Gly	Thr	Glu	Gln	Pro	Lys	Lys	Arg	Lys
1				5					10				15		

Ser	Arg	Ala	Arg	Ala	Gly	Gly	Leu	Thr	Val	Ala	Asp	Arg	Leu	Lys	Lys
							20		25			30			

20	Trp	Lys	Glu	Tyr	Asn	Glu	Ile	Val	Glu	Ala	Ser	Ala	Val	Lys	Glu
							35		40			45			

Glu	Lys	Pro	Lys	Arg	Lys	Val	Pro	Ala	Lys	Gly	Ser	Lys	Lys	Gly	Cys
						50		55			60				

Met	Lys	Gly	Lys	Gly	Gly	Pro	Asp	Asn	Ser	His	Cys	Ser	Phe	Arg	Gly
						65		70		75			80		

30	Val	Arg	Gln	Arg	Ile	Trp	Gly	Lys	Trp	Val	Ala	Glu	Ile	Arg	Glu	Pro
							85			90			95			

Lys	Ile	Gly	Thr	Arg	Leu	Trp	Leu	Gly	Thr	Phe	Pro	Thr	Ala	Glu	Lys
							100		105			110			

Ala	Ala	Ser	Ala	Tyr	Asp	Glu	Ala	Ala	Thr	Ala	Met	Tyr	Gly	Ser	Leu
							115		120		125				

40	Ala	Arg	Leu	Asn	Phe	Pro	Gln	Ser	Val	Gly	Ser	Glu	Phe	Thr	Ser	Thr
							130		135		140					

Ser	Ser	Gln	Ser	Glu	Val	Cys	Thr	Val	Glu	Asn	Lys	Ala	Val	Val	Cys
						145		150		155		160			

Gly	Asp	Val	Cys	Val	Lys	His	Glu	Asp	Thr	Asp	Cys	Glu	Ser	Asn	Pro
						165		170		175					

Phe	Ser	Gln	Ile	Leu	Asp	Val	Arg	Glu	Glu	Ser	Cys	Gly	Thr	Arg	Pro
							180		185		190				

Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr
 195 200 205
 Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln
 210 215 220
 Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Ile Gln Gln Gln Gln
 225 230 235 240
 10 Gln Glu Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala
 245 250 255
 Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser
 260 265 270
 Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu
 275 280 285
 20 Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser
 290 295 300
 Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His
 305 310 315 320
 Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
 325 330

30 (2) INFORMATION FOR SEQ ID NO.: 11:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 30

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

40 (C) OTHER INFORMATION: Designed oligonucleotide based on the
 promoter region of rd29A gene and having
 HindIII site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 11:

AAGCTTAAGC TTACATCACT TTGAAAGAAA

30

(2) INFORMATION FOR SEQ ID NO.: 12:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 31

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

10 (ix) FEATURE

(C) OTHER INFORMATION: Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 12:

AAGCTTAAGC TTGCTTTTG GAACTCATGT C

31

(2) INFORMATION FOR SEQ ID NO.: 13:

(i) SEQUENCE CHARACTERISTICS

20 (A) LENGTH: 32

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Designed oligonucleotide based on DREB1A gene and having BamHI site.

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 13:

AAGCTTAAGC TTGCCATAGA TGCAATTCAA TC

32

(2) INFORMATION FOR SEQ ID NO.: 14:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 36

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Designed oligonucleotide based on DREB1A
gene and having BamHI site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 14:

AAGCTTAAGC TTTTCCAAAG ATTTTTTCT TTCCAA

36

(2) INFORMATION FOR SEQ ID NO.: 15:

(i) SEQUENCE CHARACTERISTICS

20 (A) LENGTH: 30

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Designed oligonucleotide based on the
promoter region of rd29A gene and having

30 HindIII site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 15:

GGATCCGGAT CCATGAACTC ATTTCTGCT

30

(2) INFORMATION FOR SEQ ID NO.: 16:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 32

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 16:

GGATCCGGAT CCTTAATAAC TCCATAACGA TA

32

20 (2) INFORMATION FOR SEQ ID NO.: 17:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 941

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 17:

30 GCCATAGATG CAATTCAATC AAAC TGAAAT TTCTGCAAGA ATCTCAAACA CGGAGATCTC 60
AAAGTTGAA AGAAAATT A TTTCTTCGAC TCAAAACAAA CTTACGAAAT TTAGGTAGAA 120
CTTATATACA TTATATTGTA ATTTTTGTA ACAAAATGTT TTTATTATTA TTATAGAATT 180

TTACTGGTTA AATTAAAAAT GAATAGAAAA GGTGAATTAA GAGGAGAGAG GAGGTAAACA 240
 TTTTCTTCTA TTTTTTCATA TTTTCAGGAT AAATTATTGT AAAAGTTAC AAGATTTCCA 300
 TTTGACTAGT GTAAATGAGG AATATTCTCT AGTAAGATCA TTATTCATC TACTTCTTT 360
 ATCTTCTACC AGTAGAGGAA TAAACAATAT TTAGCTCCTT TGTAATACAA ATTAATTTT 420
 CCTTCTTGAC ATCATTCAAT TTTAATTTA CGTATAAAAT AAAAGATCAT ACCTATTAGA 480
 ACGATTAAGG AGAAATACAA TTCGAATGAG AAGGATGTGC CGTTGTTAT AATAAACAGC 540
 CACACGACGT AAACGTAAAA TGACCACATG ATGGGCAAT AGACATGGAC CGACTACTAA 600
 TAATAGTAAG TTACATTTA GGATGGAATA AATATCATA CGACATCAGT TTTGAAAGAA 660
 AAGGGAAAAA AAGAAAAAAT AAATAAAAGA TATACTACCG ACATGAGTTC CAAAAAGCAA 720
 10 AAAAAAAAGAT CAAGCCGACA CAGACACGCG TAGAGAGCAA AATGACTTTG ACGTCACACC 780
 ACGAAAACAG ACGCTTCATA CGTGTCCCTT TATCTCTCTC AGTCTCTCTA TAAACTTAGT 840
 GAGACCCCTCC TCTGTTTAC TCACAAATAT GCAAACCTAGA AAACAATCAT CAGGAATAAA 900
 GGGTTGATT ACTTCTATTG GAAAGAAAAA AATCTTTGGA A 941

(2) INFORMATION FOR SEQ ID NO.: 18:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 71

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 18:

CAGTTGAAA GAAAAGGGAA AAAAAGAAAA AATAAATAAA AGATATACTA CCGACATGAG 60

TTCCAAAAAG C

71

30 (2) INFORMATION FOR SEQ ID NO.: 19:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 71

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

.. (ii) MOLECULE TYPE: DNA

.. (vi) ORIGINAL SOURCE:

.. (A) ORGANISM: Artificial Sequence

.. (ix) FEATURE

.. (C) OTHER INFORMATION: Oligonucleotide having a partially mutated sequence within the DRE region.

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 19:

CAGTTTGAAA GAAAAGGGAA AAAAAGAAAA AATAAAATAAA AGATATATTT TCGACATGAG 60

TTCCAAAAAG C

71

(2) INFORMATION FOR SEQ ID NO.: 20:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 71

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Oligonucleotide having a partially mutated sequence within the DRE region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 20:

CAGTTTGAAA GAAAAGGGAA AAAAAGAAAA AATAAAATAAA AGATATACTA CTTTTATGAG 60

TTCCAAAAAG C

71

30

(2) INFORMATION FOR SEQ ID NO.: 21:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 71
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Artificial Sequence

(ix) FEATURE

10 (C) OTHER INFORMATION: Oligonucleotide having a partially mutated sequence within the DRE region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 21:

CAGTTTGAAA GAAAAGGGAA AAAAAGAAAA AATAAATAAA AGATATACTA CCGACAAAAAG 60
TTCCAAAAAG C

71

(2) INFORMATION FOR SEQ ID NO.: 22:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 71
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Oligonucleotide having a partially mutated sequence outside the DRE region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 22:

30 CAGTTTGAAA GAAAAGGGAA AAAAAGAAAA AATAAATAAA AGATATACTA CCGACATGAT 60
CAACAAAAAG C

71

(2) INFORMATION FOR SEQ ID NO.: 23:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 71

(B) TYPE: nucleic acid

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Artificial Sequence

(ix) FEATURE

(C) OTHER INFORMATION: Oligonucleotide having a partially mutated
sequence outside the DRE region.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 23:

CAGTTTGAAA GAAAAGGGAA AAAAAGAAAA ATATAAATAAA AGATATACTA CCGACATGAG 60

TTCGGTTAAG C

71

What is claimed is:

1. A transgenic plant containing a gene in which a DNA encoding the following protein (a) or (b) is ligated downstream of a stress responsive promoter:
 - (a) a protein consisting of the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10;
 - (b) a protein which consists of the amino acid sequence having deletion, substitution or addition of at least one amino acid in the amino acid sequence as shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8 or SEQ ID NO: 10 and which regulates the transcription of genes located downstream of a stress responsive element.
2. A transgenic plant containing a gene in which the following DNA (c) or (d) is ligated downstream of a stress responsive promoter:
 - (c) a DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9;
 - (d) a DNA which hybridizes with the DNA consisting of the nucleotide sequence as shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 or SEQ ID NO: 9 under stringent conditions and which codes for a protein that regulates the transcription of genes located downstream of a stress responsive element.
3. The transgenic plant of claim 1 or 2, wherein the stress is dehydration stress, low temperature stress or salt stress.
4. The transgenic plant of any one of claims 1 to 3, wherein the stress responsive promoter is at least one selected from the group

consisting of rd29A gene promoter, rd29B gene promoter, rd17 gene promoter, rd22 gene promoter, DREB1A gene promoter, cor6.6 gene promoter, cor15a gene promoter, erdl gene promoter and kin1 gene promoter.

Smart & Biggar
Ottawa, Canada
Patent Agents

FIG. 1

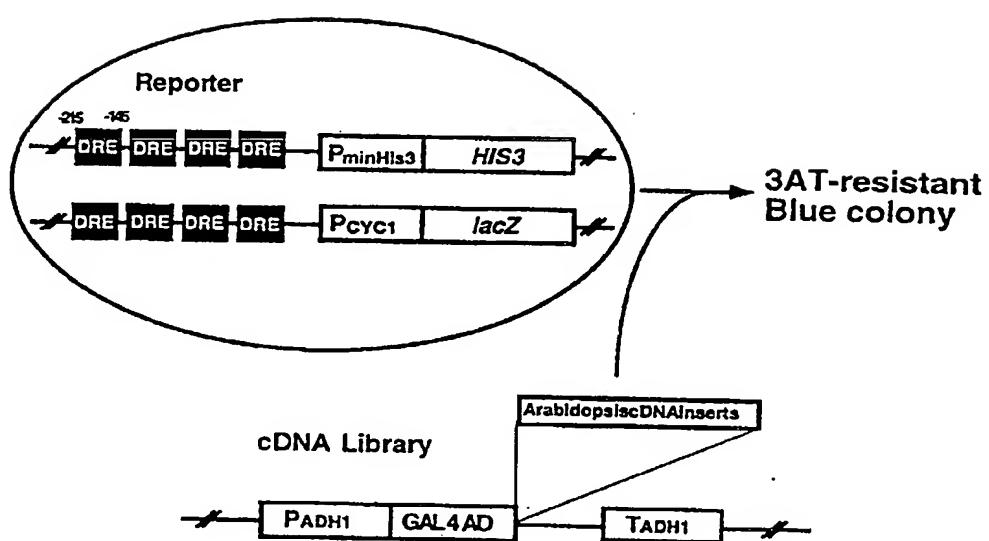


FIG. 2

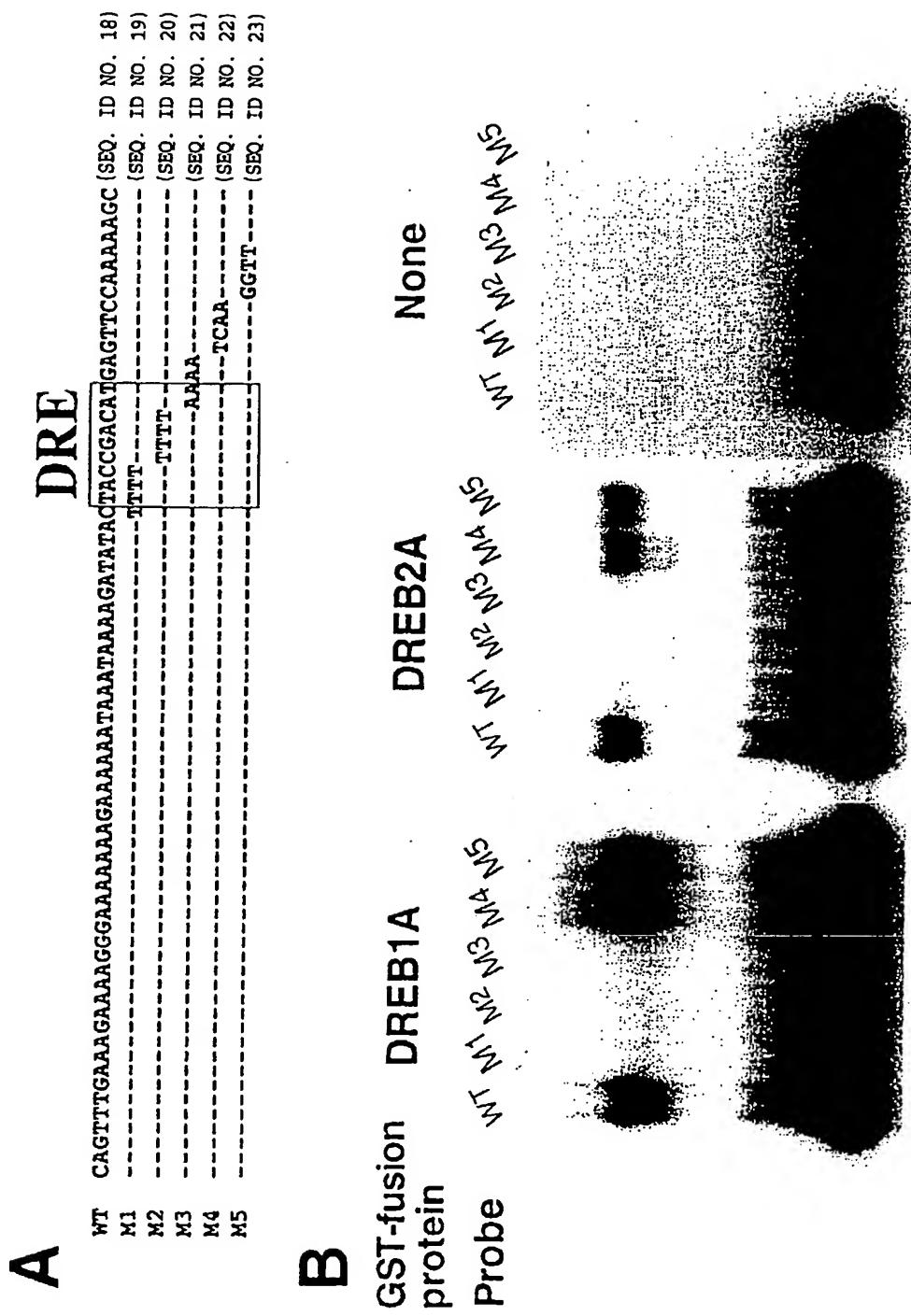
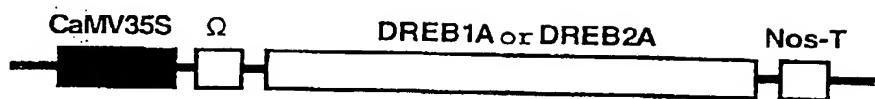


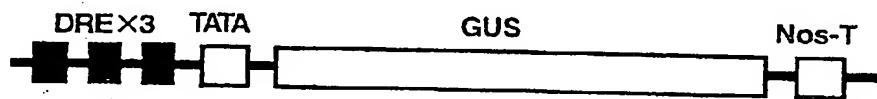
FIG. 3

A

Effector Plasmid



Reporter Plasmid



B

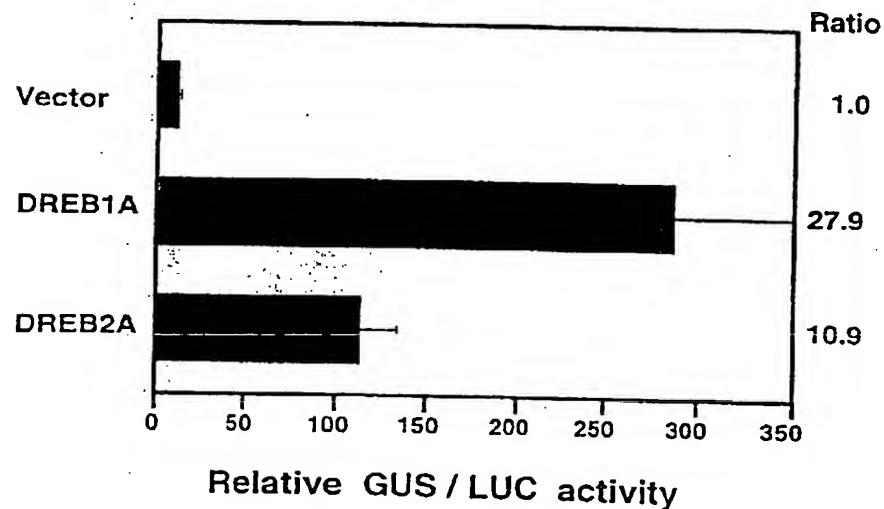


FIG. 4

35S:DREB1A

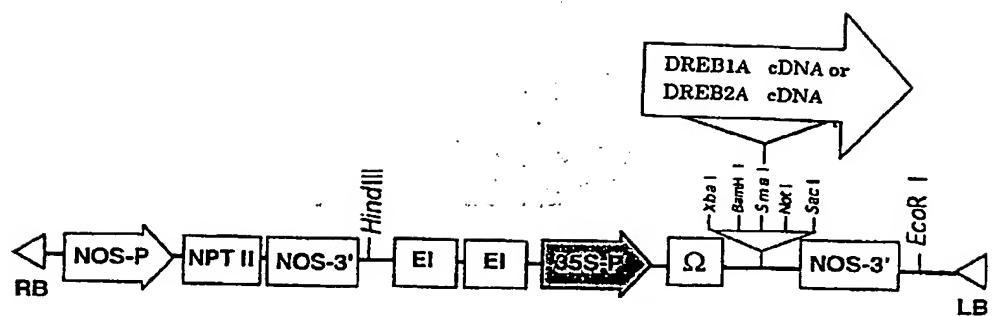


FIG. 5

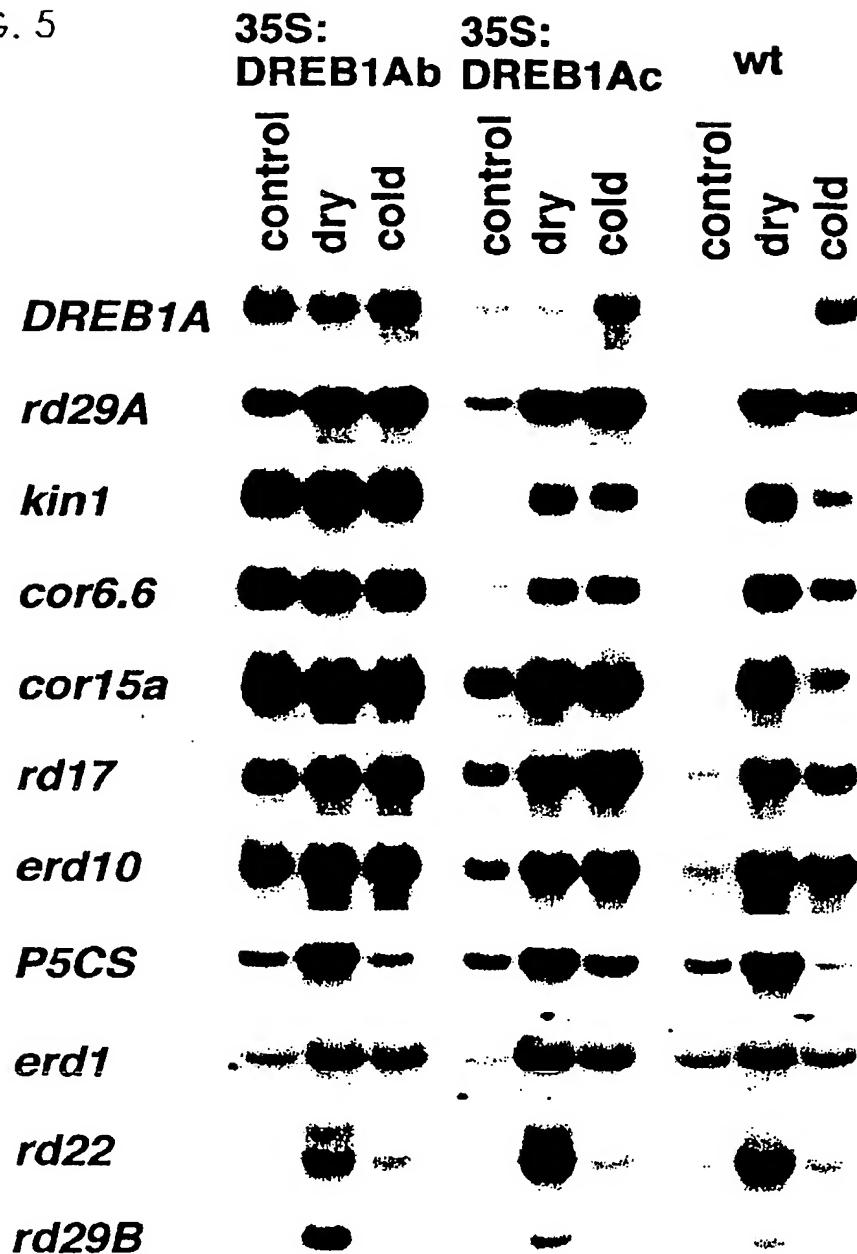


FIG. 6

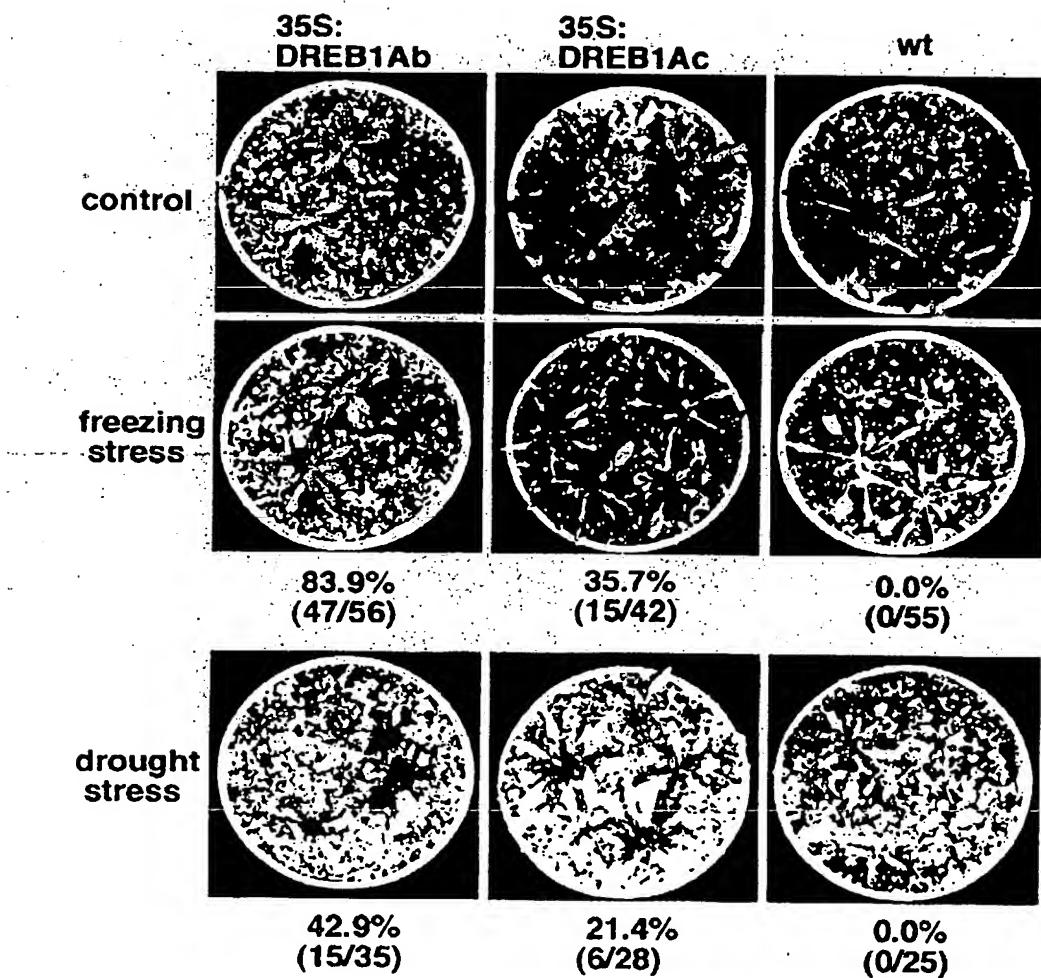


FIG. 7

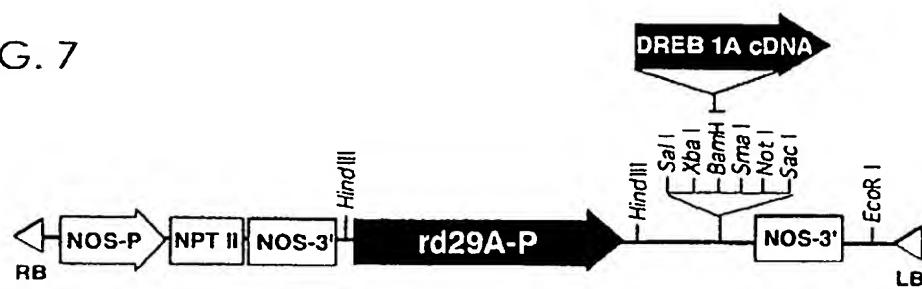


FIG. 8

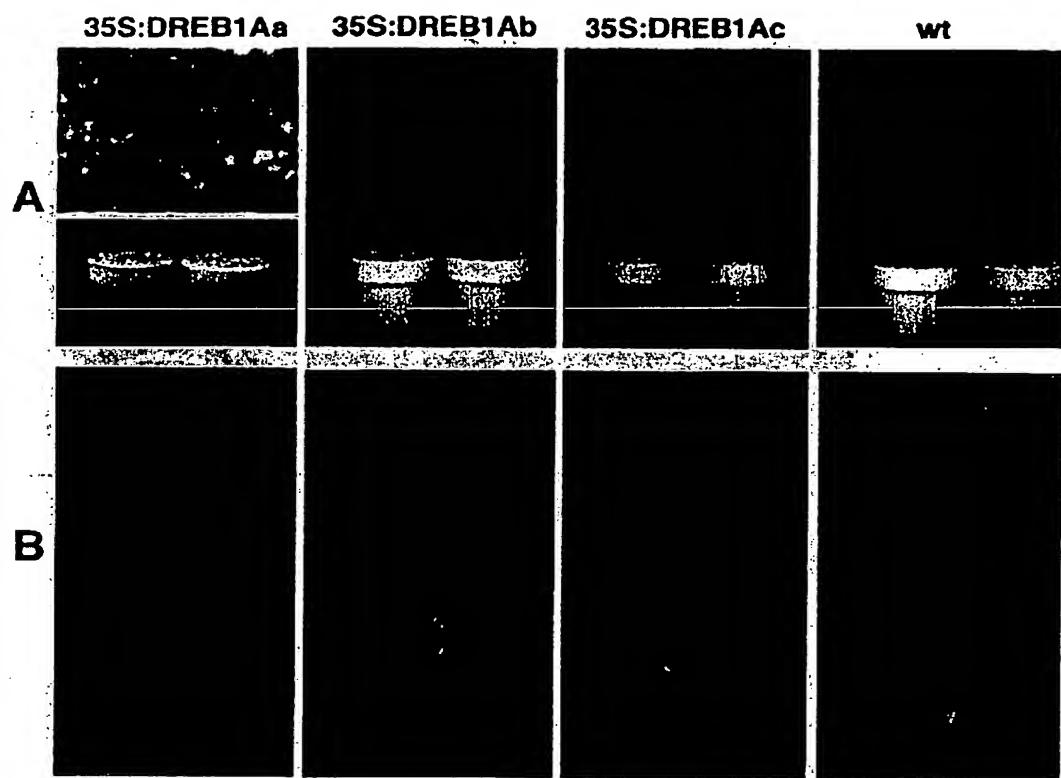


FIG. 9

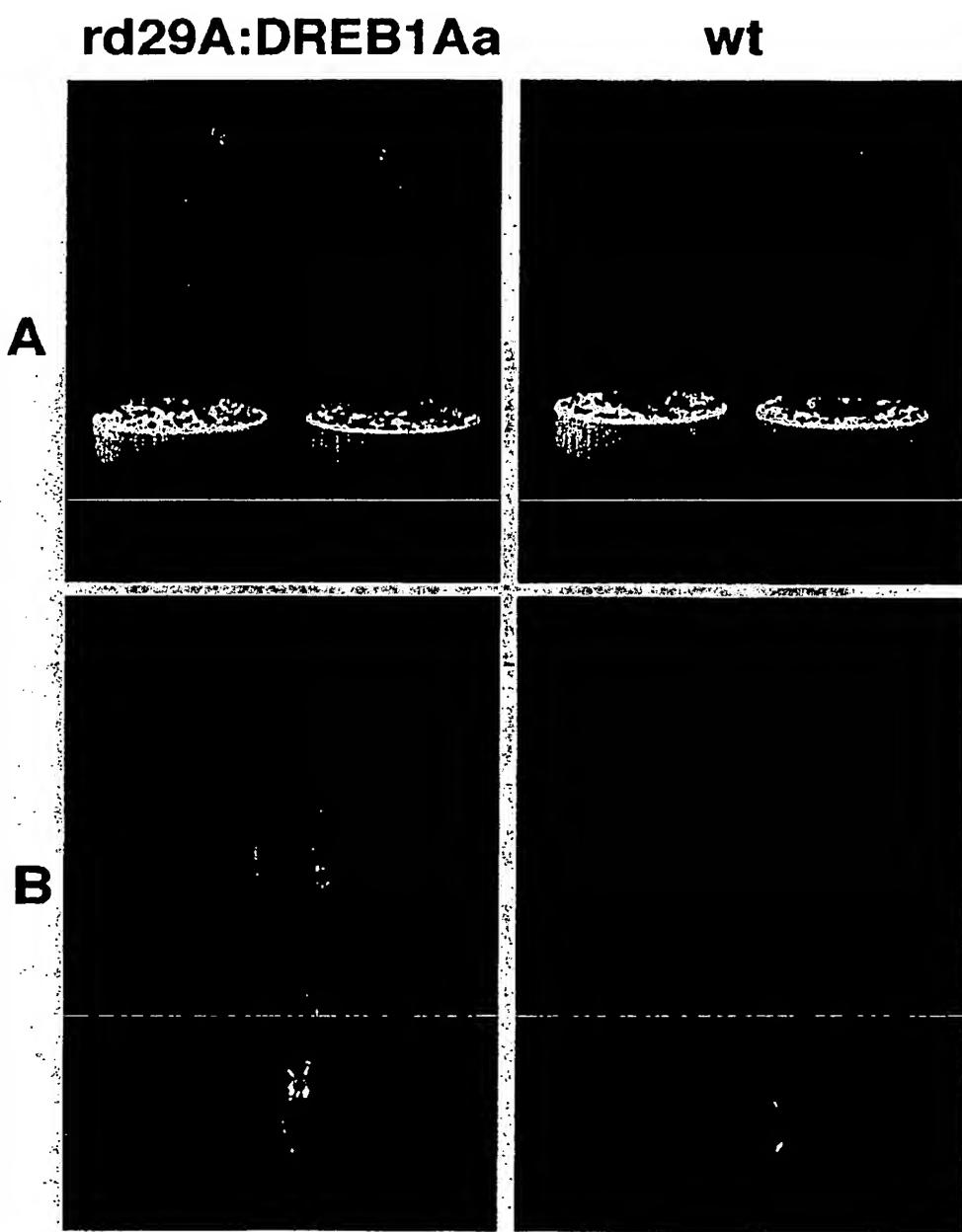
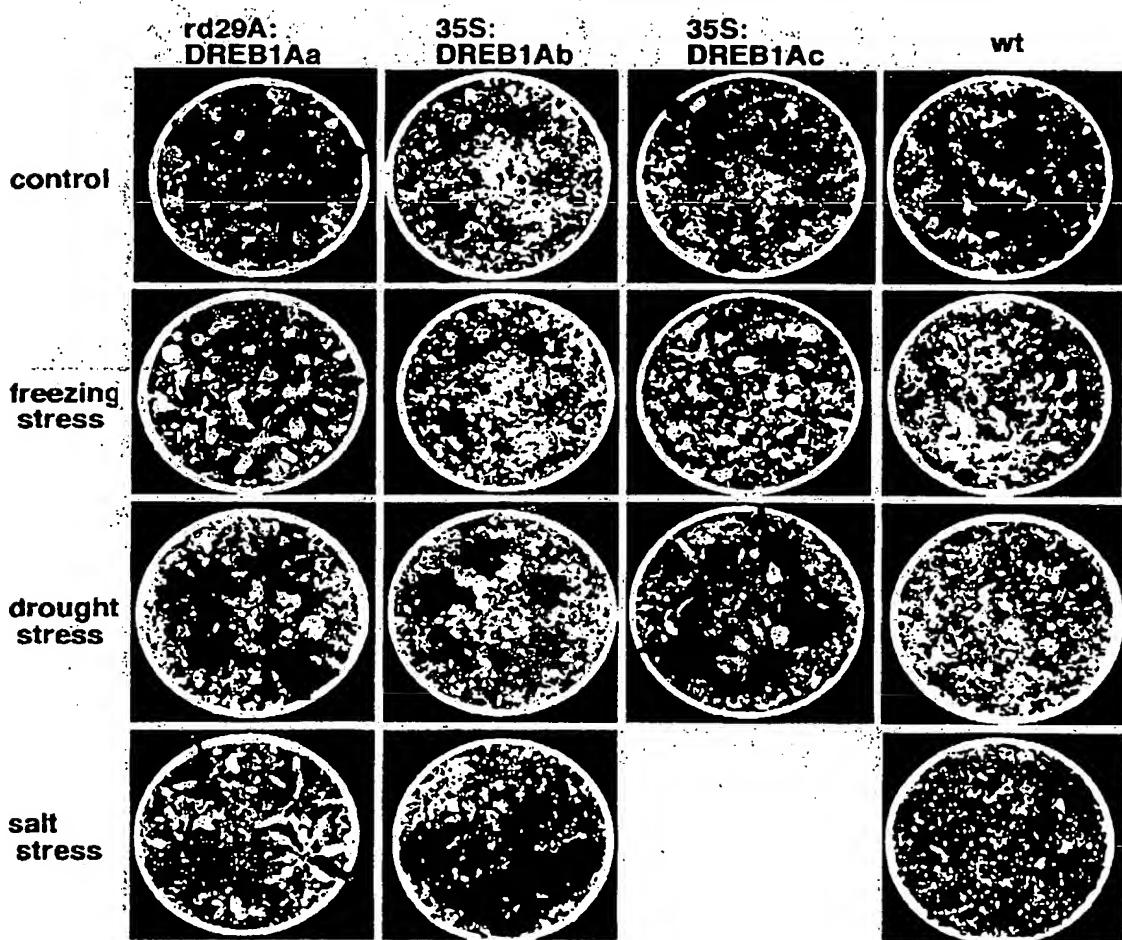


FIG. 10



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